

Result No.	Score	Query			DB	ID	Description
		Match	Length	\$			
1	800	100.0	154	4	AAy72840	Mouse Sta	
2	800	100.0	770	2	Aar72082	Mouse Sta	
3	800	100.0	770	2	AAW03176	Mouse Sta	
4	800	100.0	770	3	AAB12377	N-termina	
5	800	100.0	770	5	AAE14652	Murine ST	
6	800	100.0	770	6	ABU10476	Mouse STA	
7	792	99.0	720	5	AAE22055	Human Sta	
8	792	99.0	769	5	AB57164	Mouse lsc	
9	792	99.0	769	5	AAE22054	Human Sta	
10	792	99.0	769	5	AAE22056	Human pro	
11	792	99.0	770	2	Aar82995	Mouse liv	
12	792	99.0	770	2	AAR82993	Human pla	
13	792	99.0	770	2	AAy03768	Human STA	
14	792	99.0	770	4	AB119964	Human sig	
15	792	99.0	770	5	ABG69497	Human bai	
16	792	99.0	770	5	AAE15174	Human Sta	
17	792	99.0	770	7	ADD44738	Rat Prote	
18	792	99.0	770	7	ADD44740	Human Pro	
19	792	99.0	770	8	ADN04365	Antipsori	
20	792	99.0	770	8	ADP54789	Human PRO	
21	792	99.0	793	3	AAE58442	Lung canc	
22	380	47.5	154	4	AAY72843	Mouse Sta	
23	380	47.5	680	6	AAR59713	Human sig	
24	380	47.5	701	2	AAE41335	84 kD ISG	
25	380	47.5	701	6	ABU04741	Human exp	

CC transformation; These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain; linker domain, SH2 domain and transactivation domain
XX
SQ Sequence 154 AA;
Query Match 100.0%; Score 800; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQWNLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLIQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLIQTAA 120
QY 121 TAAQGGQGANHTAAVVTETKQOMLEQHLQDVRKR 154
DB 121 TAAQGGQGANHTAAVVTETKQOMLEQHLQDVRKR 154
RESULT 2
AAR72082
ID AAR72082 standard; protein; 770 AA.
XX
AC AAR72082;
DT 25-MAR-2003 (revised)
DT 27-SEP-1995 (first entry)
DE Mouse Stat3 (19sf6).
XX
KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
KW receptor recognition factor; transcription factor; cellular debilitation;
KW derangement; dysfunction; interferon-gamma.
XX
OS Mus sp.
XX WO9508629-A1.
XX 30-MAR-1995.
XX
PF 26-SEP-1994; 94WO-US010849.
XX
PR 24-SEP-1993; 93US-00126588.
PR 24-SEP-1993; 93US-00126595.
PR 11-MAR-1994; 94US-00212184.
PR 11-MAR-1994; 94US-00212185.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
XX
WPI: 1995-139598/18.
DR N-PSDB; AAQ89340.
XX
XX Receptor recognition factor implicated in transcriptional stimulation of
PT genes - useful in drug screening assays and/or for treating cellular
PT debilitations, derangements and/or dysfunctions, etc.
PT
PS Claim 1; Page 107-110; 160pp; English.
XX
CC A fragment encoding the human Stat91 protein was used to screen a murine
CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
CC mouse gene as probe, 2 additional members of the 113-91 family of
CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
CC and 40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-

CC 2003 to correct PN field.)
XX
SQ Sequence 770 AA;
Query Match 100.0%; Score 800; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 9e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQWNLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLIQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLIQTAA 120
QY 121 TAAQGGQGANHTAAVVTETKQOMLEQHLQDVRKR 154
DB 121 TAAQGGQGANHTAAVVTETKQOMLEQHLQDVRKR 154
RESULT 3
AAW03176
ID AAW03176 standard; protein; 770 AA.
XX
AC AAW03176;
DT 24-OCT-1996 (first entry)
XX
DE Mouse STAT4.
XX
KW STAT; STAT4; signal transducer and activator of transcription;
KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
KW autoimmune disease; antagonist; therapy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 398..508
FT /label= DNA binding domain
FT /note= "Claim 3, page 110"
XX
XX WO9620954-A2.
XX
XX 11-JUL-1996.
XX
XX 28-DEC-1995; 95WO-US017025.
XX
XX 06-JAN-1995; 95US-00369796.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Darnell JE, Wen Z, Horvath CM, Zhong Z;
XX
XX WPI: 1996-333941/33.
XX N-PSDB; AAT31280.
XX
XX New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
XX preventing or treating cellular dysfunction, e.g. oncogenesis,
XX inflammation, parasitic disease or autoimmunity.
XX
XX Disclosure; Page 87-90; 138pp; English.
XX
XX Mouse signal transducer and activator of transcription (STAT) protein
XX STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
XX ligand-activated receptor kinase complexes followed by nuclear
XX translocation and DNA binding to activate transcription. Recombinant
XX STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from
XX splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
XX AAW03167) capable of both receptor recognition and message delivery via
XX DNA binding in a receptor-ligand specific manner. STAT proteins and their
XX DNA binding domains (see also AAW03165-75) are useful for screening
XX antagonists used to inhibit STAT-mediated signal transduction and


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CC activation of transcription
XX
SQ Sequence 770 AA;

Query Match      100.0%; Score 800; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 9e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPPELQFLAPWIESQDWAYAAASKESHATLVFHNL 60
   |||||
DB 1 MAQWNLQQLDTRYLKQLHQLYSDFPPELQFLAPWIESQDWAYAAASKESHATLVFHNL 60
   |||||

QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPEIARIVARCLWEESRLLOATA 120
   |||||
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPEIARIVARCLWEESRLLOATA 120
   |||||

QY 121 TAAQGGQANHPHTAAVTEKQQLQHLQDVRKR 154
   |||||
DB 121 TAAQGGQANHPHTAAVTEKQQLQHLQDVRKR 154
   |||||

RESULT 4
AAB12377
ID AAB12377 standard; peptide; 770 AA.
XX
AC AAB12377;
XX
DT 08-NOV-2000 (first entry)
XX
DE N-terminal domain of murine STAT-3 protein.
XX
KW STAT; signal transducer and activator of transcription; crystal;
KW drug design; murine.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 4..9 /label= Alpha helix 1
FT Region 12..21 /label= Alpha helix 2
FT Region 19..21 /label= 3(10) helix of alpha helix 2
FT Region 28..33 /label= Alpha helix 3
FT Region 35..40 /label= Alpha helix 4
FT Region 43..47 /label= Alpha helix 5
FT Region 50..73 /label= Alpha helix 6
FT Region 77..96 /label= Alpha helix 7
FT Region 99..119 /label= Alpha helix 8
XX
XX US6087478-A.
XX
XX 11-JUL-2000.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX
XX WPI; 2000-505108/45.
XX
XX New crystals of an N-terminal fragment of a signal transducer and
XX activator of transcription that effectively diffracts x-rays, useful for
XX drug screening and development.
XX

XX Disclosure; Fig 1; 42pp; English.
XX
CC The present invention relates to a crystal of an N-terminal fragment of a
CC signal transducer and activator of transcription (STAT) protein. The
CC crystal effectively diffracts x-rays, allowing the determination of the
CC atomic coordinates of the N-terminal domain to a resolution of greater
CC than 5.0 Angstroms. The present sequence is the N-terminal domain of the
CC murine STAT 3 protein. The N-terminal domain enables STAT dimers to
CC interact and bind DNA cooperatively, a mechanism important for gene
CC activation. The crystals are useful in drug screening and development by
CC selecting a potential drug by performing rational drug design with the 3-
CC dimensional structure determined for the crystal
XX
SQ Sequence 770 AA;

Query Match      100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 9e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPPELQFLAPWIESQDWAYAAASKESHATLVFHNL 60
   |||||
DB 1 MAQWNLQQLDTRYLKQLHQLYSDFPPELQFLAPWIESQDWAYAAASKESHATLVFHNL 60
   |||||

QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPEIARIVARCLWEESRLLOATA 120
   |||||
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPEIARIVARCLWEESRLLOATA 120
   |||||

QY 121 TAAQGGQANHPHTAAVTEKQQLQHLQDVRKR 154
   |||||
DB 121 TAAQGGQANHPHTAAVTEKQQLQHLQDVRKR 154
   |||||

RESULT 5
AAB14652
ID AAB14652 standard; protein; 770 AA.
XX
AC AAB14652;
XX
DT 16-JUL-2002 (first entry)
XX
DE Murine STAT3 protein.
XX
KW Signal transducer and activator of transcription; STAT3;
KW drug development; drug discovery; crystal; inflammation; allergy; asthma;
KW leukaemia; anaemia; neutropenia; thrombocytopaenia; cancer; obesity;
KW viral disease; growth retardation; murine.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 1..130 /note= "Conserved N-terminal domain of the STAT family"
FT FT
XX
XX US6312887-B1.
XX
XX 06-NOV-2001.
XX
XX 24-APR-2000; 2000US-00556273.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX
XX WPI; 2002-033337/04.
XX
XX Identifying compounds that bind to signal transducer and activator of
XX transcription proteins, useful for the production of new drugs.
XX
XX Example; Col 47-50; 44pp; English.
XX

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CC The invention relates to methods for detecting compounds that bind to
 CC signal transducer and activator of transcription (STAT) proteins for the
 CC discovery and development of new drug compounds based on the structural
 CC properties of the protein crystal. The methods include: identifying a
 CC compound that binds to the N-terminal domain of a STAT protein,
 CC identifying a compound that enhances or diminishes the binding of the
 CC dimeric STAT proteins to each other and/or their nucleic acid binding
 CC site; or identifying a compound that enhances or diminishes the ability
 CC of STAT protein dimers to induce the expression of a gene operably under
 CC the control of a promoter containing at least two adjacent weak binding
 CC sites for STAT protein dimers. The methods are used for identifying new
 CC drugs. An antagonist of STAT N-terminal dimeric interactions that
 CC inhibits the binding of the STAT dimers to adjacent weak binding sites on
 CC a promoter of a gene, could be useful as drugs in the treatment of
 CC diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other
 CC hand, an agonist of N-terminal dimeric interactions between STAT dimers,
 CC can be used as drugs in the treatment of diseases e.g. anaemia,
 CC neutropenia, thrombocytopaenia, cancer, obesity, viral diseases and
 CC growth retardation. The present sequence is murine STAT3 protein
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 800; DB 5; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9e-77; Indels 0; Gaps 0;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 QY 61 LGEIDQOYSRFLQESNVLVYQHNLRIKQFLQSRYLEKPMIARIVARCLWEESRLLOQTAA 120
 DB 61 LGEIDQOYSRFLQESNVLVYQHNLRIKQFLQSRYLEKPMIARIVARCLWEESRLLOQTAA 120
 QY 121 TAAQGGQGANHPHTAAVVTKEQQLMEOHLOQDVRRK 154
 DB 121 TAAQGGQGANHPHTAAVVTKEQQLMEOHLOQDVRRK 154

RESULT 6
 ABU10476
 ID ABU10476 standard; protein; 770 AA.
 XX
 AC ABU10476;
 DT 06-AUG-2003 (first entry)
 XX
 DE Mouse STAT3 protein..
 XX
 KW Mouse; signal transducer and activator of transcription; drug design;
 KW drug screening; STAT-STAT dimer interaction; STAT3.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 4..9 /label= alpha_helix_1
 FT Region 12..21 /label= alpha_helix_2
 FT /note= "Residues 19-21 form a 3 helix"
 FT Region 28..33 /label= alpha_helix_3
 FT Region 35..40 /label= alpha_helix_4
 FT Region 43..47 /label= alpha_helix_5
 FT Region 50..73 /label= alpha_helix_6
 FT /note= "Residues 57, 61, 64, 68 and 71 contribute to
 FT packing of the coiled-coil"
 FT Region 77..96 /label= alpha_helix_7
 FT /note= "Residues 79, 83, 86, 90 and 94 contribute to

FT packing of the coiled-coil"
 FT 99..119 /label= alpha_helix_8
 XX
 PN US2003003563-A1.
 XX
 PD 02-JAN-2003.
 XX
 XX 19-OCT-2001; 2001US-00045792.
 XX
 XX 23-JAN-1998; 98US-00012710.
 PR 24-APR-2000; 2000US-00556273.
 XX
 PA (VINK/) VINKEMEIER U.
 PA (MOAR/) MOAREFI I.
 PA (DARN/) DARNELL J E.
 PA (KURI/) KURIYAN J.
 XX
 FI Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
 XX
 XX WPI; 2003-447354/42.
 DR
 XX
 PT New crystal having an N-terminal domain of a STAT protein performing X-
 PT ray crystallographic studies, useful for screening drugs that enhance or
 PT inhibit STAT-STAT dimer interactions.
 XX
 PS Disclosure; Page 25-36; 46pp; English.
 XX
 CC The invention relates to a crystal of an N-terminal domain of signal
 CC transducer and activator of transcription (STAT) protein, where the
 CC crystal effectively diffracts X-rays for the determination of the atomic
 CC coordinates of the N-terminal domain of the STAT protein to a resolution
 CC of greater than 5.0 Angstrom. The methods and compositions are useful for
 CC the design and screening of drugs that enhance or inhibit STAT-STAT dimer
 CC interactions. The present sequence represents the amino acid sequence of
 CC mouse STAT3 protein
 XX
 SQ Sequence 770 AA;
 Query Match 100.0%; Score 800; DB 6; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9e-77; Indels 0; Gaps 0;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 QY 61 LGEIDQOYSRFLQESNVLVYQHNLRIKQFLQSRYLEKPMIARIVARCLWEESRLLOQTAA 120
 DB 61 LGEIDQOYSRFLQESNVLVYQHNLRIKQFLQSRYLEKPMIARIVARCLWEESRLLOQTAA 120
 QY 121 TAAQGGQGANHPHTAAVVTKEQQLMEOHLOQDVRRK 154
 DB 121 TAAQGGQGANHPHTAAVVTKEQQLMEOHLOQDVRRK 154
 RESULT 7
 AAEE22055
 ID AAEE22055 standard; protein; 720 AA.
 XX
 AC AAEE22055;
 DT 25-JUL-2002 (first entry)
 XX
 DE Human Stat3beta protein.
 XX
 KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;

KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.
 XX Homo sapiens.
 OS
 PH Key Location/Qualifiers
 FT Misc-difference 713..714
 FT /note="Encoded by ACA CCA TTC"
 PN W0200220032-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028254.
 XX
 PR 08-SEP-2000; 2000US-0231212P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Yu H, Pardoll D, Jove R, Dalton W;
 XX
 DR WPI; 2002-362218/39.
 DR N-PSDB; AAD35066.
 XX
 PT Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX
 PS Disclosure; Page 87-89; 94pp; English.
 XX
 CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g. bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC Stat3beta protein
 XX
 SQ Sequence 720 AA;
 Query Match 99.0%; Score 792; DB 5; Length 720;
 Best Local Similarity 98.7%; Pred. No. 6e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 DB 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRRRIKQFLQSYLEKPMIARIARCLWEESRLLOTAA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRRIKQFLQSYLEKPMIARIARCLWEESRLLOTAA 120
 QY 121 TAAQGGGQANHTAAVVTKEQKQMLQHLQDVRKR 154
 DB 121 TAAQGGGQANHTAAVVTKEQKQMLQHLQDVRKR 154
 RESULT 8
 ABB57164
 ID ABB57164 standard; protein; 769 AA.
 XX
 AC ABB57164;
 XX
 DT 07-MAR-2002 (first entry)
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:398.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX
 OS Mus musculus.
 XX
 PN W0200188188-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-JP004192.
 XX
 PR 18-MAY-2000; 2000JP-00145977.
 XX
 PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 DR WPI; 2002-034733/04.
 DR N-PSDB; ABI19454.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX
 PS Claim 2; Page 1084-1087; 2690pp; English.
 XX
 CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (i) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (i). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI199202 to ABI19912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI19913 and ABI19914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 769 AA;
 Query Match 99.0%; Score 792; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 6.5e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 DB 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRRIKQFLQSYLEKPMIARIARCLWEESRLLOTAA 120

PT compound that modulates the activity of a signal transducer and activator
 of transcription 3.

XX Disclosure; Page 83-85; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 response. Method involves administering to an individual a compound that
 modulate the activity of signal transducer and activator of transcription
 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation

XX SQ Sequence 769 AA;

Query Match 99.08; Score 792; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 6.5e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQNNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 DB 1 MAQNNQLQQLDTRYLEQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
 QY 121 TAAQGGQGANHPHTAAVTEKQMLQHLQDVRRK 154
 DB 121 TAAQGGQGANHPHTAAVTEKQMLQHLQDVRRK 154

RESULT 11

AAR82995
 ID AAR82995 standard; protein; 770 AA.

XX AAR82995;

XX 25-MAR-1996 (first entry)

XX Mouse liver acute phase response factor.

XX Mouse; acute phase response factor; transcription factor; interleukin-6;
 KW signal transmission; liver; antibody; antisense; ribozyme;
 KW antiinflammatory; antitumor; hypotensive; therapy.

XX Mus musculus.

XX EP676469-A2.

XX 11-OCT-1995.

XX

PF 29-MAR-1995; 95EP-00104670.

PR 04-APR-1994; 94JP-00065825.

XX (KISH/) KISHIMOTO T.

XX Akira S, Kishimoto T;

XX WPI; 1995-346089/45.

DR N-PSDB; AAT05619.

XX New acute phase response factor - for developing inhibitory agents for
 treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
 diseases.

XX Claim 10; Page 20-22; 31pp; English.

XX The sequence represents a mouse acute phase response factor (APRF), a
 transcription factor related to signal transmission of interleukin-6 (IL-
 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
 library using a polymerase chain reaction product (amplified using
 CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
 CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
 CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
 CC inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
 CC hypertension, etc

XX SQ Sequence 770 AA;

Query Match 99.0%; Score 792; DB 2; Length 770;
 Best Local Similarity 98.7%; Pred. No. 6.5e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQNNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 DB 1 MAQNNQLQQLDTRYLEQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
 QY 121 TAAQGGQGANHPHTAAVTEKQMLQHLQDVRRK 154
 DB 121 TAAQGGQGANHPHTAAVTEKQMLQHLQDVRRK 154

RESULT 12

AAR82993
 ID AAR82993 standard; protein; 770 AA.

XX AAR82993;

XX 25-MAR-1996 (first entry)

XX Human placenta acute phase response factor protein.

XX human; acute phase response factor; transcription factor; interleukin-6;
 KW signal transmission; placenta; antibody; antisense; ribozyme;
 KW antiinflammatory; antitumor; hypotensive; therapy.

XX Homo sapiens.

XX EP676469-A2.

XX 11-OCT-1995.

XX 29-MAR-1995; 95EP-00104670.

XX 04-APR-1994; 94JP-00065825.

XX (KISH/) KISHIMOTO T.

XX Akira S, Kishimoto T;

XX

```
XX DR WPI; 1995-346089/45.
XX DR N-PSDB; AAT05616.
XX PT New acute phase response factor - for developing inhibitory agents for
XX PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
XX PT diseases.
XX PS Claim 3; Page 9-12; 31pp; English.
XX CC The sequence corresponds to a human acute phase response factor (APRF), a
XX CC transcription factor related to signal transmission of interleukin-6 (IL-
XX CC 6). The protein is expressed from a human placenta cDNA, isolated using
XX CC an IL-6-treated mouse liver cDNA probe. APRF-inhibitors, e.g. antibodies,
XX CC antisense oligonucleotides or ribozymes, may be used to treat diseases
XX CC induced by IL-6, e.g. inflammatory disease, leukemia, cancer,
XX CC osteoclasia, pulmonary hypertension, etc
XX SQ Sequence 770 AA;
Query Match 99.0%; Score 792; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 6.5e-76;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQWNQLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Qy 61 LGEIDQOYSRFLQSNVLYOHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOTTAA 120
Db 61 LGEIDQOYSRFLQSNVLYOHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOTTAA 120
Qy 121 TAAQGGQGANHPTAAVVTKEQQLQHLQDVRKR 154
Db 121 TAAQGGQGANHPTAAVVTKEQQLQHLQDVRKR 154
RESULT 13
AAY03768
ID AAY03768 standard; protein; 770 AA.
XX AC AAY03768;
XX DT 11-JUN-1999 (first entry)
XX DE Human STAT3 allelic variant.
XX KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
XX KW intracellular transcription factor; interleukin-6; medicament; variant;
XX KW pharmaceutical; autoimmune disease; inflammatory; human.
XX OS Homo sapiens.
XX PN EP05234-A2.
XX PD 31-MAR-1999.
XX PF 18-FEB-1998; 98EP-00102774.
XX PR 16-SEP-1997; 97EP-00116061.
XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PI Serlupi-Crescenzi O, Della Pietra L;
XX DR WPI; 1999-192664/17.
XX DR N-PSDB; AAX29281.
XX PT New human Signal Transducer and Activator of Transcription 3 (STAT3)
XX PT allelic variant useful for treatment of autoimmune and inflammatory
XX PT disease.
XX PS Claim 2; Page 9-13; 32pp; English.
XX CC The present sequence represents a predominant allelic variant of human
XX CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
XX CC intracellular transcription factor which mediates IL-6 signals. The
XX CC encoding sequence differs from the original published human STAT3 gene
XX CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
XX CC DNA molecule can be used for the recombinant expression of the variant.
XX CC STAT3 protein is useful as a medicament or pharmaceutical composition for
XX CC treatment of autoimmune or inflammatory diseases
XX SQ Sequence 770 AA;
Query Match 99.0%; Score 792; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 6.5e-76;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQWNQLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Qy 61 LGEIDQOYSRFLQSNVLYOHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOTTAA 120
Db 61 LGEIDQOYSRFLQSNVLYOHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOTTAA 120
Qy 121 TAAQGGQGANHPTAAVVTKEQQLQHLQDVRKR 154
Db 121 TAAQGGQGANHPTAAVVTKEQQLQHLQDVRKR 154
RESULT 14
AAB19964
ID AAB19964 standard; protein; 770 AA.
XX AC AAB19964;
XX DT 28-MAR-2001 (first entry)
XX DE Human signal transducer and activator of transcription STAT-3.
XX KW STAT-3; signal transducer and activator of transcription 3; human;
XX KW crystal; drug screening.
XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT Domain 134..320
XX FT /note= "coiled-coil domain"
XX FT Domain 321..493
XX FT /note= "DNA-binding domain"
XX FT Domain 494..583
XX FT /note= "linker domain"
XX FT Domain 584..688
XX FT /note= "SH2 domain"
XX FT Region 689..717
XX FT /note= "C-terminal tail segment"
XX FT Modified-site 705
XX FT /note= "O-phosphorylated"
XX PN US6160092-A.
XX PD 12-DEC-2000.
XX PF 29-MAY-1998; 98US-00087465.
XX PR 29-MAY-1998; 98US-00087465.
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PI Chen X, Darnell JE, Kuriyan J, Vinkemeier U, Zhao Y, Jeruzalmi D;
XX PI WPI; 2001-101568/11.
XX DR N-PSDB; AAB89229.
XX XX
```

PT Novel crystal useful in drug screening assays, comprises portion of
PT signal transducer, activator of transcription and duplex DNA.
XX
PS Disclosure; Col 67-71; 206pp; English.

XX The present sequence is that of human signal transducer and activator of
CC transcription 3 (STAT-3). The invention provides a crystal of a core
CC portion of a STAT protein in dimer form with an 18-mer duplex DNA (see
CC AAA89233) that contains a binding site for the STAT dimer. The core
CC portion comprises a coiled-coil domain comprising 4 long helices, a DNA
CC binding domain which contains an immunoglobulin-like fold, a C-terminal
CC SH2 domain and a domain that links the DNA binding and SH2 domains. The
CC crystal is of sufficient quality to perform X-ray crystallography
CC studies. Methods of preparing the crystals are included in the invention.
CC Knowledge of the STAT protein's 3-dimensional structure will aid in
CC structure-based drug design. The crystal can be used in drug screening
CC assays to identify agonist and antagonist compounds. Antagonists can be
CC used to treat inflammation, allergy, asthma and leukaemia, and agonists
CC to treat anaemia, neutropenia, thrombocytopenia, cancer, obesity, viral
CC diseases, growth retardation, and other conditions characterized by
CC insufficient STAT activity
XX

SQ Sequence 770 AA;

Query Match 99.0%; Score 792; DB 4; Length 770;
Best Local Similarity 98.7%; Pred. No. 6.5e-76;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQHLQHSYDTPFMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
DB 1 MAQWNLQQLDTRYLKQHLQHSYDTPFMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMPIARIVARCLWEESRLQTA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMPIARIVARCLWEESRLQTA 120
QY 121 TAAQGGQANHPHTAAVVTTEKQMLEQHLQDVRRK 154
DB 121 TAAQGGQANHPHTAAVVTTEKQMLEQHLQDVRRK 154

RESULT 15

ABG69497
ID ABG69497 standard; protein; 770 AA.

AC ABG69497;

DT 21-OCT-2002 (first entry)

XX Human bait protein STAT3.

XX Human; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;

KW non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
KW protein-protein interaction map; PWM; anorectic; metabolic disorder.

XX Homo sapiens.

XX WO200253726-A2.

XX 11-JUL-2002.

XX 28-DEC-2001; 2001WO-EP015423.

XX 02-JAN-2001; 2001US-0259377P.

XX (HYBR-) HYBRIGENICS.

PA (CNRS) CENT NAT RECH SCI.

XX Legrain P, Marullo S, Jockers R;

XX WPI; 2002:583612/62.

DR N-PSDB; ABS51033.

XX

PT Novel complex of protein-protein interactions in adipocyte cells for
PT identifying compounds that modulate the protein-protein interactions and
XX useful for treating obesity and metabolic disorders.

PS Claim 1; Page 54; 125pp; English.

XX The invention relates to a complex of protein-protein interactions
CC (forming a protein-protein interaction map, PWM) in adipocyte cells as
CC defined in the specification, or polynucleotides in adipocytes encoding the
CC for the polypeptides. Also included are a recombinant cell expressing the
CC interacting polypeptides and a method of selecting a modulating compound
CC in adipocyte cells, by cultivating a recombinant host cell on a selective
CC medium containing a modulating compound and a reporter gene the
CC expression of which is toxic for the recombinant host cell which is
CC transformed with two vectors, where the first vector comprises a
CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain
CC and the second vector comprising a polynucleotide encoding a second
CC hybrid polypeptide and an activating domain that activates the toxic
CC reporter gene, when the first and second hybrid polypeptides interact and
CC selecting the modulating compound which inhibits the growth of the
CC recombinant host cell (i.e. using the yeast two-hybrid system). The
CC complexes are useful for identifying compounds that modulate the protein-
CC protein interactions and useful for treating obesity and metabolic
CC disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
CC compound isolated by the method is useful for treating and preventing
CC obesity or metabolic diseases. The interactions between the proteins of
CC the complex further define a set of selected interacting domains, SID.
CC The present sequence represents a member of the protein complex of the
CC invention, used as the bait protein in the yeast two-hybrid assay
XX
SQ Sequence 770 AA;

Query Match 99.0%; Score 792; DB 5; Length 770;
Best Local Similarity 98.7%; Pred. No. 6.5e-76;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQHLQHSYDTPFMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
DB 1 MAQWNLQQLDTRYLKQHLQHSYDTPFMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMPIARIVARCLWEESRLQTA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMPIARIVARCLWEESRLQTA 120
QY 121 TAAQGGQANHPHTAAVVTTEKQMLEQHLQDVRRK 154
DB 121 TAAQGGQANHPHTAAVVTTEKQMLEQHLQDVRRK 154

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Job time : 50.8306 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 14:55:35 ; Search time 23.1306 Seconds
(without alignments)
495.716 Million cell updates/sec

Title: US-10-090-185-8

Perfect score: 800

Sequence: 1 MAQWNLQQLDTRYLKQLHQ.....AVTEKQOMLEQLQDVKR 154

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	800	100.0	154	3	US-09-387-418A-8
2	800	100.0	770	1	US-08-369-796-12
3	800	100.0	770	2	US-08-852-091-12
4	800	100.0	770	2	US-08-820-754-12
5	800	100.0	770	3	US-08-956-652-12
6	800	100.0	770	3	US-08-956-869-12
7	800	100.0	770	3	US-09-012-710-8
8	800	100.0	770	3	US-08-948-547-12
9	800	100.0	770	3	US-09-364-970-3
10	800	100.0	770	3	US-09-364-970-5
11	800	100.0	770	3	US-09-556-273-8
12	800	100.0	770	3	US-08-956-653A-12
13	800	100.0	770	4	US-08-212-185-12
14	800	100.0	770	5	PCT-US95-17025-12
15	792	99.0	770	1	US-08-416-581B-1
16	792	99.0	770	1	US-08-416-581B-5
17	792	99.0	770	1	US-08-416-581B-9
18	792	99.0	770	3	US-03-087-465-6
19	792	99.0	770	3	US-09-526-542-2
20	792	99.0	770	4	US-09-972-800A-6
21	792	99.0	770	4	US-10-117-087-2
22	792	99.0	771	1	US-08-276-099A-14
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25	380	47.5	712	1	US-08-369-796-6
26	380	47.5	712	1	US-08-852-091-6
27	380	47.5	712	2	US-08-820-754-6

28	380	47.5	712	3	US-08-956-652-6	Sequence 6, Appli
29	380	47.5	712	3	US-08-956-869-6	Sequence 6, Appli
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31	380	47.5	712	3	US-08-956-653A-6	Sequence 6, Appli
32	380	47.5	712	4	US-08-212-185-6	Sequence 2, Appli
33	380	47.5	712	4	US-09-430-806A-2	Sequence 6, Appli
34	380	47.5	712	5	PCT-US95-17025-6	Sequence 6, Appli
35	380	47.5	729	4	US-09-917-254-97	Sequence 97, Appli
36	380	47.5	740	1	US-08-276-099A-12	Sequence 12, Appli
37	380	47.5	740	1	US-08-781-890-12	Sequence 12, Appli
38	380	47.5	750	1	US-08-369-796-4	Sequence 4, Appli
39	380	47.5	750	2	US-08-852-091-4	Sequence 4, Appli
40	380	47.5	750	2	US-08-820-754-4	Sequence 4, Appli
41	380	47.5	750	3	US-08-956-652-4	Sequence 4, Appli
42	380	47.5	750	3	US-08-956-869-4	Sequence 4, Appli
43	380	47.5	750	3	US-08-948-547-4	Sequence 4, Appli
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45	380	47.5	750	3	US-09-364-970-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-387-418A-8
; Sequence 8, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-8

Query Match 100.0%; Score 800; DB 3; Length 154;

Best Local Similarity 100.0%; Pred. No. 7.3e-79;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNLQQLDTRYLKQLHOLYSDFPMEIRQFLAPWIESQDWAYAAKESHATLVFHNL 60

Db 1 MAQWNLQQLDTRYLKQLHOLYSDFPMEIRQFLAPWIESQDWAYAAKESHATLVFHNL 60

Qy 61 LGEDIQOYSFLOESNVLYOHNLRRIRKQFLQSRVLEKPMETARIVARCLWEESRLLOTAA 120

Db 61 LGEDIQOYSFLOESNVLYOHNLRRIRKQFLQSRVLEKPMETARIVARCLWEESRLLOTAA 120

Qy 121 TAAQGGQANHPTAAVVTEKQOMLEQLQDVKR 154

Db 121 TAAQGGQANHPTAAVVTEKQOMLEQLQDVKR 154

RESULT 2

US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622

; GENERAL INFORMATION:

; APPLICANT: James E. Darnell, Jr.

; APPLICANT: Zilong Wen

; APPLICANT: Curt M. Horvath

; APPLICANT: Zhong Zhong

; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL

; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS

```
;
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 343-1684
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-369-796-12

Query Match 100.0%; Score 800; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHNL 60

Qy 61 LGEDIQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEDIQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPTAAVVTKEQOMLEQHLQDVVRK 154
Db 121 TAAQGGQANHPTAAVVTKEQOMLEQHLQDVVRK 154

RESULT 3
US-08-852-091-12
; Sequence 12, Application US/08852091
; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-852-091-12

Query Match 100.0%; Score 800; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHNL 60

Qy 61 LGEDIQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEDIQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPTAAVVTKEQOMLEQHLQDVVRK 154
Db 121 TAAQGGQANHPTAAVVTKEQOMLEQHLQDVVRK 154

RESULT 4
US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,754
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
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; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-820-754-12

Query Match 100.0%; Score 800; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
DB 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
QY 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
DB 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
QY 121 TAAQGGQANHPTAAVTEKQMLEQHLQDVYRKR 154
DB 121 TAAQGGQANHPTAAVTEKQMLEQHLQDVYRKR 154

RESULT 5
US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,652
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-652-12

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
DB 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
QY 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
DB 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
QY 121 TAAQGGQANHPTAAVTEKQMLEQHLQDVYRKR 154
DB 121 TAAQGGQANHPTAAVTEKQMLEQHLQDVYRKR 154

RESULT 6
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; QUERY MATCH 100.0%; Score 800; DB 3; Length 770;
; Best Local Similarity 100.0%; Pred. No. 5.9e-78;
; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
; DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
; QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOTAA 120
; DB 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOTAA 120
; QY 121 TAAQGGQGANHTAAVTEKQQLMEOHLOQDVRRK 154
; DB 121 TAAQGGQGANHTAAVTEKQQLMEOHLOQDVRRK 154
;
; RESULT 7
; US-09-012-710-8
; Sequence 8, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moareff, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; NUMBER OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; QUERY MATCH 100.0%; Score 800; DB 3; Length 770;
; Best Local Similarity 100.0%; Pred. No. 5.9e-78;
; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
; DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
; QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOTAA 120
; DB 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOTAA 120
; QY 121 TAAQGGQGANHTAAVTEKQQLMEOHLOQDVRRK 154
; DB 121 TAAQGGQGANHTAAVTEKQQLMEOHLOQDVRRK 154
;
; RESULT 8
; US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
Db 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60

Qy 61 LGEIDQYSRFLQSSNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQSSNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTKEQKQMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQKQMLEQHLQDVRRK 154

RESULT 9

US-09-364-970-3
Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-3

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
Db 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60

Qy 61 LGEIDQYSRFLQSSNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQSSNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTKEQKQMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQKQMLEQHLQDVRRK 154

RESULT 10

US-09-364-970-5
Sequence 5, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-5

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
Db 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60

Qy 61 LGEIDQYSRFLQSSNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQSSNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTKEQKQMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQKQMLEQHLQDVRRK 154

RESULT 11

US-09-556-273-8
Sequence 8, Application US/09556273
Patent No. 6312887
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Darneil, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-556-273-8

Query Match          100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNQLQQDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQANHPHTAAVVTKEQMLQHLQDVRKR 154
DB 121 TAAQGGQANHPHTAAVVTKEQMLQHLQDVRKR 154

RESULT 12
US-08-956-653A-12
; Sequence 12, Application US/08956653A
; Patent No. 6338949
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,653A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:

; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; MISMATCHES: 0; Gaps 0;
Indels 0; Gaps 0;
Query Match          100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNQLQQDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQANHPHTAAVVTKEQMLQHLQDVRKR 154
DB 121 TAAQGGQANHPHTAAVVTKEQMLQHLQDVRKR 154

RESULT 13
US-08-212-185-12
; Sequence 12, Application US/08212185
; Patent No. 6605442
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO US93/02569
;; FILING DATE: 19-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/126,588
;; FILING DATE: 24-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-17025-12
US-08-212-185-12

Query Match      100.0%; Score 800; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQNNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
Db 1 MAQNNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTXKQMLEQHLQDVKR 154
Db 121 TAAQGGQANHPHTAAVVTXKQMLEQHLQDVKR 154

RESULT 14
PCT-US95-17025-12
Sequence 12, Application PC/TUS9517025
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17025
FILING DATE: 28-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
```

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;; REFERENCE/DOCKET NUMBER: 600-1-116
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-17025-12
US-08-416-581B-1

Query Match      100.0%; Score 800; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQNNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
Db 1 MAQNNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTXKQMLEQHLQDVKR 154
Db 121 TAAQGGQANHPHTAAVVTXKQMLEQHLQDVKR 154

RESULT 15
US-08-416-581B-1
Sequence 1, Application US/08416581B
Patent No. 5719042
GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamoto
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-37891
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-416-581B-1
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Query Match      99.0%; Score 792; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 4.3e-77;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MAQWNLQQLDTRYLEQLHQLYSDTFPMELKQFLAPWIESQDWAYAAKESHATLVFHNL 60

Qy      61 LGEIDQOYSRFLQSNVLYQHNLRRIKQFLQSRYLEKPEIARIVARCLWEESRLLOTAA 120
Db      61 LGEIDQOYSRFLQSNVLYQHNLRRIKQFLQSRYLEKPEIARIVARCLWEESRLLOTAA 120

Qy      121 TAAQGGQGANHPTAAVVTEKQOMLEQHLQDVYRKR 154
Db      121 TAAQGGQGANHPTAAVVTEKQOMLEQHLQDVYRKR 154

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Search completed: May 5, 2005, 14:58:51
Job time : 26.1906 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 14:59:00 ; Search time 64.8612 Seconds
(without alignments)
792.064 Million cell updates/sec

Title: US-10-090-185-8
Perfect score: 800
Sequence: 1 MAQWNQLQDLTRYLKQLH.....AVTEKQOMLEQLHLDVRKR 154

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	800	100.0	154	13 US-10-090-185-8	Sequence 8, Appli
2	800	100.0	770	11 US-09-876-773-6	Sequence 12, Appli
3	800	100.0	770	14 US-10-045-792-8	Sequence 8, Appli
4	800	100.0	770	17 US-10-639-617-12	Sequence 12, Appli
5	792	99.0	720	15 US-10-380-020-4	Sequence 4, Appli
6	792	99.0	769	15 US-10-380-020-2	Sequence 2, Appli
7	792	99.0	769	15 US-10-380-020-5	Sequence 5, Appli
8	792	99.0	770	14 US-10-038-010-56	Sequence 56, Appli
9	792	99.0	770	14 US-10-117-087-2	Sequence 2, Appli
10	792	99.0	770	15 US-10-116-275-329	Sequence 329, App
11	792	99.0	770	15 US-10-116-275-349	Sequence 349, App
12	792	99.0	793	9 US-09-925-302-780	Sequence 780, App
13	792	99.0	793	10 US-09-925-302-780	Sequence 780, App

14	380	47.5	154	13	US-10-090-185-11	Sequence 11, Appli
15	380	47.5	712	11	US-09-876-773-6	Sequence 6, Appli
16	380	47.5	712	14	US-10-245-120-2	Sequence 2, Appli
17	380	47.5	712	17	US-10-639-617-6	Sequence 6, Appli
18	380	47.5	712	17	US-10-936-390-5	Sequence 5, Appli
19	380	47.5	750	9	US-09-833-205-2	Sequence 2, Appli
20	380	47.5	750	11	US-09-876-773-4	Sequence 4, Appli
21	380	47.5	750	14	US-10-245-120-1	Sequence 1, Appli
22	380	47.5	750	14	US-10-308-279-44	Sequence 44, Appli
23	380	47.5	750	16	US-10-755-889-352	Sequence 352, App
24	380	47.5	750	16	US-10-755-889-823	Sequence 823, App
25	380	47.5	750	17	US-10-492-043-19	Sequence 19, Appli
26	380	47.5	750	17	US-10-639-617-4	Sequence 4, Appli
27	380	47.5	786	9	US-09-925-297-550	Sequence 550, App
28	378	47.2	749	9	US-09-833-205-4	Sequence 6, Appli
29	378	47.2	749	9	US-09-833-205-6	Sequence 8, Appli
30	378	47.2	749	11	US-09-876-773-8	Sequence 7, Appli
31	378	47.2	749	14	US-10-045-792-7	Sequence 39, Appli
32	378	47.2	749	14	US-10-205-194-39	Sequence 8, Appli
33	378	47.2	749	17	US-10-639-617-8	Sequence 4, Appli
34	360	45.0	131	14	US-10-245-120-4	Sequence 10, Appli
35	334.5	41.8	748	11	US-09-876-773-10	Sequence 10, Appli
36	334.5	41.8	748	17	US-10-639-617-10	Sequence 9, Appli
37	334.5	41.8	749	14	US-10-045-792-9	Sequence 437, App
38	333.5	41.7	423	14	US-10-177-293-437	Sequence 439, App
39	333.5	41.7	748	14	US-10-177-293-439	Sequence 70, Appli
40	333.5	41.7	748	16	US-10-755-889-70	Sequence 389, App
41	333.5	41.7	748	16	US-10-755-889-362	Sequence 389, App
42	247.5	30.9	532	14	US-10-205-823-389	Sequence 2, Appli
43	247.5	30.9	851	11	US-09-876-773-2	Sequence 2, Appli
44	247.5	30.9	851	14	US-10-045-792-2	Sequence 2, Appli
45	247.5	30.9	851	15	US-10-179-451-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-090-185-8
; Sequence 8, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR E
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-8

Query Match 100.0%; Score 800; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. NO. 4.7e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQDLTRYLKQLHLYSDTFPMELRQFLAPMIESQDWAYAAKESHATLVFHNL 60
Db 1 MAQWNQLQDLTRYLKQLHLYSDTFPMELRQFLAPMIESQDWAYAAKESHATLVFHNL 60
Qy 61 LGEDIQYSRFLQBSNVLYQHNLRRIKQFLQSRVLEKPMELRIVARCLWEESRLQTAA 120
Db 61 LGEDIQYSRFLQBSNVLYQHNLRRIKQFLQSRVLEKPMELRIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPTAAVVTEKQOMLEQHLQDVKR 154
121 TAAQGGQANHPTAAVVTEKQOMLEQHLQDVKR 154

RESULT 2
US-09-876-773-12
Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

	Query Match	100.0%;	Score 800;	DB 11;	Length 770;
	Best Local Similarity	100.0%;	Pred. No. 3.7e-76;		
	Matches 154;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAOWNQLQDLTRYLKHLYSTDFPMEIHFQFLAPWIESODWAYAAKESHATLVFHNL	60		
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Qy	61	LGETDQQYSRFLQSNNVLYQHNLRRIRIKOFTLOSRYLEKPMEIARIVARCLWEESKLLOTA	120		
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QY      121 TAAQGGQANHPTAAVVTKEQOMLEQHLQDYRK 154
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DB      121 TAAQGGQANHPTAAVVTKEQOMLEQHLQDYRK 154
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RESULT 3
US-10-045-792-8
; Sequence 8, Application US/10045792
; Publication NO. US20030003563A1
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
;           Mearefi, Ismail
;           Darnell, Jr., James E.
;           Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Eq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-10-045-792-8

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Db	1	MAQWNLQQLDTRYLYKQLHQLYSDTTPMEIARQFLAPWIE	SQDWAYAASKESHATLVFNHL	60
Qy	61	LGEIDQOYGRFLOESNVLYOHNLRRIKQFLQSYLEKPM	IAIRIVARCLWBEESLLQTA	120
Db	61	LGEIDQOYGRFLOESNVLYOHNLRRIKQFLQSYLEKPM	IAIRIVARCLWBEESLLQTA	120
Qy	121	TAAQCGQGANHPATAAVVTEKQOMLEHQLQDVVRKR		154
Db	121	TAAQCGQGANHPATAAVVTEKQOMLEHQLQDVVRKR		154

Qy 121 TAAQGGQANHPTAAVVTEKQMLEQHLQDVKR 154
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Db 121 TAAQGGQANHPTAAVVTEKQMLEQHLQDVKR 154

RESULT 4

US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/639,617
; FILING DATE: 12-Aug-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 100.0%; Score 800; DB 17; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.7e-76;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHQLYSTFPFMELRQFLAPWIESQDWAYAAASKESHATLVFPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSTFPFMELRQFLAPWIESQDWAYAAASKESHATLVFPHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
Qy 121 TAAQCGQGANHTAAVVTKEQKMLEQHLQDVKRK 154
Db 121 TAAQCGQGANHTAAVVTKEQKMLEQHLQDVKRK 154

RESULT 5

US-10-380-020-4
; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match 99.0%; Score 792; DB 15; Length 720;
Best Local Similarity 98.7%; Pred. No. 2.4e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHQLYSTFPFMELRQFLAPWIESQDWAYAAASKESHATLVFPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSTFPFMELRQFLAPWIESQDWAYAAASKESHATLVFPHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
Qy 121 TAAQCGQGANHTAAVVTKEQKMLEQHLQDVKRK 154
Db 121 TAAQCGQGANHTAAVVTKEQKMLEQHLQDVKRK 154

RESULT 6

US-10-380-020-2
; Sequence 2, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT<
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match 99.0%; Score 792; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAQWNQLQQLDTRYLKQLHQLYSTFPFMELRQFLAPWIESQDWAYAAASKESHATLVFPHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120

Db 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Qy 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 7
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match 99.0%; Score 792; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEIRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEIRQFLAPWIESQDWAYAASKESHATLVPHNL 60

Qy 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 8
US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56

Query Match 99.0%; Score 792; DB 14; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEIRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEIRQFLAPWIESQDWAYAASKESHATLVPHNL 60

Qy 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 9
US-10-117-087-2
; Sequence 2, Application US/10117087
; Publication No. US20030166854A1
; GENERAL INFORMATION:
; APPLICANT: SERLUPI-CRESCENZI, Ottaviano
; APPLICANT: DELLA PIETRA, Linda
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REFERENCE: SERLUPI=2
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2

Query Match 99.0%; Score 792; DB 14; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEIRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEIRQFLAPWIESQDWAYAASKESHATLVPHNL 60

Qy 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 10
US-10-116-275-329
; Sequence 329, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 329
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Rat
US-10-116-275-329

Query Match          99.0%; Score 792; DB 15; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
Db 1 MAQWNQLQQLDTRYLYEQHLQHSYSPFMLELQFLAPWIESQDWAYAAKESHATLVFHNL 60

Qy 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154

RESULT 11
US-10-116-275-349
; Sequence 349, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116.275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 349
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-349

Query Match          99.0%; Score 792; DB 15; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
Db 1 MAQWNQLQQLDTRYLYEQHLQHSYSPFMLELQFLAPWIESQDWAYAAKESHATLVFHNL 60

Qy 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154

RESULT 12
US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925.302
```

```
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match          99.0%; Score 792; DB 9; Length 793;
Best Local Similarity 98.7%; Pred. No. 2.8e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
Db 24 MAQWNQLQQLDTRYLYEQHLQHSYSPFMLELQFLAPWIESQDWAYAAKESHATLVFHNL 83

Qy 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 84 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 143

Qy 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154
Db 144 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 177

RESULT 13
US-09-925-302-780
; Sequence 780, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925.302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match          99.0%; Score 792; DB 10; Length 793;
Best Local Similarity 98.7%; Pred. No. 2.8e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
Db 24 MAQWNQLQQLDTRYLYEQHLQHSYSPFMLELQFLAPWIESQDWAYAAKESHATLVFHNL 83

Qy 61 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 84 LGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 143

Qy 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154
Db 144 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 177

RESULT 14
US-10-090-185-11
; Sequence 11, Application US/10090185
; Publication No. US20020197647A1
```

GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 154
TYPE: PRT
ORGANISM: Mus musculus
US-10-090-185-11

Query Match 47.5%; Score 380; DB 13; Length 154;
Best Local Similarity 44.8%; Pred. No. 2.5e-32;
Matches 69; Conservative 42; Mismatches 41; Indels 2; Gaps 1;
Qy 1 MAOWNQLQQLDTRYLKHQHYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MSQWYELQQLDQSKLEQVHQLYDSDSPFMEIRQYLAQWLEKQDWEHAANDYSFATIRFHD 60
Qy 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LSQDDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Qy 121 TAAQGGQANHTAAVTEKQMLEQHLQDVVKR 154
Db 121 RFNQ--AQSGNIQSTVMDKQKELDSKVRNVKDK 152

RESULT 15

US-09-876-773-6
Sequence 6, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992

APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 712 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-876-773-6

Query Match 47.5%; Score 380; DB 11; Length 712;
Best Local Similarity 44.8%; Pred. No. 1.8e-31;
Matches 69; Conservative 42; Mismatches 41; Indels 2; Gaps 1;
Qy 1 MAOWNQLQQLDTRYLKHQHYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MSQWYELQQLDQSKLEQVHQLYDSDSPFMEIRQYLAQWLEKQDWEHAANDYSFATIRFHD 60
Qy 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LSQDDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Qy 121 TAAQGGQANHTAAVTEKQMLEQHLQDVVKR 154
Db 121 RFNQ--AQSGNIQSTVMDKQKELDSKVRNVKDK 152

Search completed: May 5, 2005, 15:17:40
Job time : 65.8612 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2005, 14:55:35 ; Search time 11.2329 Seconds
(without alignments)
1319.101 Million cell updates/sec

Title: US-10-090-185-8

Perfect score: 800

Sequence: 1 MAQWNQLQDLTRYLKQLHQ.....AVVTEKQMLEHQLQDVKKR 154

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: piri:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792	99.0	770	2 A54444	DNA-binding protei
2	792	99.0	770	2 I49508	ISGF3 p91-related
3	380	47.5	739	2 A46159	interferon-depende
4	334.5	41.8	748	2 A56047	gamma-interferon a
5	247.5	30.9	851	2 A46160	interferon alpha-1
6	188	23.5	786	2 I49274	mammary gland fact
7	187	23.4	794	2 G02317	transcription acti
8	186	23.2	793	2 S54772	mammary gland fact
9	147.5	18.4	794	2 S55527	mammary gland fact
10	98	12.2	331	2 A10354	probable lipoprote
11	97	12.1	837	2 I57557	DNA-Binding Protei
12	91.5	11.4	848	2 A54740	interleukin-4-indu
13	88	11.0	1355	2 T22552	hypothetical prote
14	82.5	10.3	371	2 T40287	hypothetical prote
15	82.5	10.3	373	2 F71884	probable lipopolys
16	82	10.2	498	2 C69587	L-arabinose isomer
17	82	10.2	620	2 S56790	probable membrane
18	82	10.2	764	2 C83513	hypothetical prote
19	81.5	10.2	276	2 H81707	inclusion membrane
20	81	10.1	2954	2 T14156	kinesin-related pr
21	80.5	10.1	1110	2 A43253	Large tra-1 protei
22	80	10.0	508	1 KXSHB2	keratin type II, m
23	79.5	9.9	392	2 T19867	hypothetical prote
24	79.5	9.9	444	2 E30192	DNA repair protein
25	79.5	9.9	613	2 S48557	hypothetical prote
26	79.5	9.9	638	2 I53169	cytokeatin 2 - hu
27	79.5	9.9	4957	2 T03455	ALR protein - huma
28	79.5	9.9	5262	2 T03454	ALR protein - huma
29	79	9.9	4540	2 T30838	cytoplasmic dynein

30 78.5 9.8 1033 2 S73593 MG328 homolog p01-
31 78.5 9.8 2101 2 A42184 nuclear mitotic ap
32 78.5 9.8 2168 2 T30171 ninein - mouse
33 78 9.8 409 2 F71956 hypothetical prote
34 78 9.8 629 2 A29666 keratin, 65K type
35 78 9.8 1462 2 T00345 hypothetical prote
36 77.5 9.7 2133 2 T30637 hypothetical prote
37 77 9.6 191 2 AB2247 hypothetical prote
38 77 9.6 2160 2 T20241 hypothetical prote
39 76.5 9.6 625 2 T37604 probable transcrip
40 76 9.5 390 2 A72108 hypothetical prote
41 76 9.5 390 2 B86514 hypothetical prote
42 76 9.5 442 2 C83192 conserved hypothet
43 76 9.5 812 2 T34180 hypothetical prote
44 75.5 9.4 895 2 T13414 probable alpha-act
45 75.5 9.4 924 2 T13413 probable alpha-act

ALIGNMENTS

RESULT 1

A54444

DNA-binding protein APRF - human

C:Species: Homo sapiens (man)

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C:Accession: A54444

R:Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud

Cell 77, 63-71, 1994

A:Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra

A:Reference number: A54444; MUID:94208062; PMID:7512451

A:Accession: A54444

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-770 <RES>

A:Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789

C:Genetics:

A:Gene: GDB:STAT3; APRF

A:Cross-references: GDB:358950

A:Map position: 17q21-17q21

C:Superfamily: human signal transducer and transcription activator STAT5A

C:Keywords: DNA binding; transcription factor

Query Match 99.0%; Score 792; DB 2; Length 770;

Best Local Similarity 98.7%; Pred. No. 1.1e-61;

Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQDLTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60

Db 1 MAQWNQLQDLTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60

Qy 61 LGEDIQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLMEESRLQTA 120

Db 61 LGEDIQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLMEESRLQTA 120

Qy 121 TAAQGGQGANHTAAVVTETKQMLEHQLQDVKKR 154

Db 121 TAAQGGQGANHTAAVVTETKQMLEHQLQDVKKR 154

RESULT 2

I49508

ISGF3 p91-related transcription factor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49508; I49009

R:Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud

Cell 77, 63-71, 1994

A:Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra

A:Reference number: A54444; MUID:94208062; PMID:7512451

A:Accession: I49508

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P42227; GB:L292278; NID:G476715; PIDN:AAA37254.1; PID:G476716
R;Raz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
A;Title: Acute phase response factor and additional members of the interferon-stimulated
A;Reference number: I49009; MUID:95014185; PMID:7523373
A;Accession: I49009
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-393, 'M', 395-700, 702-770 <RE2>
A;Cross-references: EMBL:U08378; NID:G473889; PIDN:AAA56668.1; PID:G473890
C;Genetics:
A;Gene: APRF
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 99.0%; Score 792; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 1.1e-61;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQHLQYSDTPPMEIRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQHLQYSDTPPMEIRQFLAPWIESQDWAYAAKESHATLVFHNL 60
QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
DB 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQANHTAAVTEKQMLEQHLQDVVR 154
DB 121 TAAQGGQANHTAAVTEKQMLEQHLQDVVR 154

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 47.5%; Score 380; DB 2; Length 739;
Best Local Similarity 44.8%; Pred. No. 1.5e-25;
Matches 69; Conservative 42; Mismatches 41; Indels 2; Gaps 1;

QY 1 MAQWNLQQLDTRYLKQHLQYSDTPPMEIRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MSQWYELQQLDTSKLEQVHQLYDSDTPPMEIRQFLAPWIESQDWAYAAKESHATLVFHNL 60
QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
DB 61 LSQLDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQANHTAAVTEKQMLEQHLQDVVR 154
DB 121 RFNO--AQSGNIQSTVMDKQKLEDSKVRNVKDK 152

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, J.
Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in ear
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:G509502; PIDN:AAA19692.1; PID:G509503
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 41.8%; Score 334.5; DB 2; Length 748;
Best Local Similarity 41.4%; Pred. No. 1.5e-21;
Matches 63; Conservative 38; Mismatches 50; Indels 1; Gaps 1;

QY 1 MAQWNLQQLDTRYLKQHLQYSDTPPMEIRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MSQWYELQQLDTSKLEQVHQLYDSDTPPMEIRQFLAPWIESQDWAYAAKESHATLVFHNL 60
QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
DB 61 LQIDQQLGRVSKKKNLLIHLNKRIRKVLQGFHGNPMHVAVVISNCLREERRIL-AAA 119
QY 121 TAAQGGQANHTAAVTEKQMLEQHLQDVVR 152
DB 120 NMPIQGLEKSLQSSSVSRQRNVKHSVSAIK 151

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
N;Alternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator,
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-851 <FU1>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
submitted to the EMBL Data Library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:G1293919; PIDN:AAA98760.1; PID:G1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
A;Reference number: S53873; MUID:95192056; PMID:7885841
A;Accession: S53873
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-196;392-591;684-730 <YAM>
A;Cross-references: EMBL:U18671
C;Genetics:
A;Gene: stat2
A;Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 40/2;
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: signal transduction; transcription regulation

Query Match 30.9%; Score 247.5; DB 2; Length 851;
Best Local Similarity 37.6%; Pred. No. 7.5e-14;
Matches 59; Conservative 34; Mismatches 55; Indels 9; Gaps 6;


```
Qy 1 MAQWNLQQLDTRYLKQLHQLYSDT-PPMELRQFLAPWIESQDWAYAA--SKESHATLVF 57
Db 1 MAQWNLQQLDTRYLKQLHQLYSDT-PPMELRQFLAPWIESQDWAYAA--SKESHATLVF 60
Qy 58 HNLGELIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELRQFLAPWIESQDWAYAA--ASKESHATLV 116
Db 61 FHFLDQLNYECGRCSQDPESLLOHNLKFKCRDQIP-FSQDPTQLAEMIFNLLLEEXKIL 119
Qy 117 QTAATAAQCGQANHPPTAAVVTEKQ-MLEQHLQDVR 152
Db 120 IQAORAQLEQGE---PVLTEPVESQOHEIESRIILDLR 153

RESULT 6
149274
mammary gland factor - mouse
N:Alternate names: STAT5 protein homolog p80
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R:Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved i
A:Reference number: 149273; MUID:96004632; PMID:7568026
A:Accession: 149274
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-786 <RES>
A:Cross-references: UNIPROT:P42232; UNIPROT:O9JWK1; EMBL:U21110; NID:g747973; PIDN:AAC52
R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A:Reference number: S54772; MUID:95237198; PMID:7720707
A:Accession: S54773
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-432, 'E', 434-786 <MUI>
A:Cross-references: EMBL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R:Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A:Title: Interleukin-3 signals through multiple isoforms of Stat5.
A:Reference number: S54725; MUID:95246733; PMID:7537213
A:Accession: S54727
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-432, 'E', 434-786 <AZA>
C:Genetics:
A:Gene: Stat5b
C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 23.5%; Score 188; DB 2; Length 786;
Best Local Similarity 30.1%; Pred. No. 1.1e-08;
Matches 47; Conservative 26; Mismatches 75; Indels 8; Gaps 2;

Qy 1 MAQWNLQQLDTRYLKQLHQLYSDT-PPMELRQFLAPWIESQDWAYAA--ASKESHATLV 56
Db 1 MAMWIAQQLQGDALHQMQLYGHQFFPIEVRYHLYAQMIESQDWAYAIDLDNPDQRAQATOL 60
Qy 57 FHNLLGEIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELRQFLAPWIESQDWAYAA--ASKESHATLV 116
Db 61 LEGVLQELQKKAHQVGDGFLKIKLGHYATQISTYDRCPMELVRCIRHILYNEORLV 120
Qy 117 QTAATAAQCGQANHPPTAAVVTEKQMLEQHLQDVR 152
Db 121 REANNSSPAGS----LADAMSQKHILQINQTFEELR 152

RESULT 7
G02317
transcription activator stat5a - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G02317
```

```
R:Lin, J.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01043
A:Accession: G02317
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-794 <LIN>
A:Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g115
C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 23.4%; Score 187; DB 2; Length 794;
Best Local Similarity 31.4%; Pred. No. 1.4e-08;
Matches 48; Conservative 23; Mismatches 68; Indels 14; Gaps 3;

Qy 1 MAQWNLQQLDTRYLKQLHQLYSDT-PPMELRQFLAPWIESQDWAYAA--ASKESHATLV 56
Db 1 MAGWIAQQLQGDALHQMQLYGHQFFPIEVRYHLYAQMIESQDWAYAIDLDNPDQRAQATOL 60
Qy 57 FHNLLGEIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELRQFLAPWIESQDWAYAA--ASKESHATLV 116
Db 61 LEGVLQELQKKAHQVGDGFLKIKLGHYATQISTYDRCPMELVRCIRHILYNEORLV 120
Qy 117 QTAATAAQCGQANHPPTAAVVTEKQMLEQHLQ 149
Db 121 REA-----NNCSPAGILV---DAMSQKHILQ 143

RESULT 8
S54772
mammary gland factor - mouse
N:Alternate names: stat5 protein
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S54772; I49273
R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A:Reference number: S54772; MUID:95237198; PMID:7720707
A:Accession: S54772
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-793 <MUI>
A:Cross-references: UNIPROT:P42230; UNIPROT:O9JJA0; EMBL:Z48538; NID:g758633; PIDN:CAA88
R:Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved i
A:Reference number: 149273; MUID:96004632; PMID:7568026
A:Accession: 149273
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-793 <RES>
A:Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972
C:Genetics:
A:Gene: Stat5a
C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 23.2%; Score 186; DB 2; Length 793;
Best Local Similarity 29.5%; Pred. No. 1.7e-08;
Matches 46; Conservative 26; Mismatches 76; Indels 8; Gaps 2;

Qy 1 MAQWNLQQLDTRYLKQLHQLYSDT-PPMELRQFLAPWIESQDWAYAA--ASKESHATLV 56
Db 1 MAGWIAQQLQGDALHQMQLYGHQFFPIEVRYHLYAQMIESQDWAYAIDLDNPDQRAQATOL 60
Qy 57 FHNLLGEIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELRQFLAPWIESQDWAYAA--ASKESHATLV 116
Db 61 LEGVLQELQKKAHQVGDGFLKIKLGHYATQISTYDRCPMELVRCIRHILYNEORLV 120
Qy 117 QTAATAAQCGQANHPPTAAVVTEKQMLEQHLQDVR 152
Db 121 REANNSSPAG-----VLVDAMSQKHILQINQTFEELR 152
```

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Db 187 NL-----LDTRKLENLTDIERQLSSRKQLQNEIPETDAAEAKSAEAQNQPAAKPA 241
Qy 139 EKQ 141
   | :
Db 242 ESK 244
   | :

RESULT 11
157557
DNA-Binding Protein and transcription factor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I57557
R:Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.
Mol. Cell. Biol. 15, 3336-3343, 1995
A:Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosin
A:Reference number: I57557; MUID:95280934; PMID:7760829
A:Accession: I57557
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-837 <RES>
A:Cross-references: UNIPROT:P52633; GB:L47650; NID:g1008876; PIDN:AAA79006.1; E
C:Genetics:
C:Gene: STAT6
C:Superfamily: human signal transducer and transcription activator STAT5A

      12.1%; Score 97; DB 2; Length 837;
      Best Local Similarity 24.8%; Pred. No. 1.2;
      Matches 29; Conservative 21; Mismatches 55; Indels 12; Gaps 4
Qy 1 MAQWNLQGLDTRLYKQLHQLYSDTFPEMLQFLPWTESODYAAASKESHATLVFPHNL 60
Db 1 MSLWGLISKMSp---EXKLQRLYVD-FPQRLHLADWLQSPWEFLVGSDFCYNMASAL 56
Qy 61 LGEIDQQYSRFLQE---SNVLYQHNLRRIKQFLOSRLYLEKPEMEIARIIVARCLWEESR 114
Db 57 LSATVQRIQATAGQKGNLSLPH-----ISTLSIYORDPLKLVATRIILQEGKK 108

```

```

RESULT 12
A54740
interleukin-4-induced transcription factor stat - human
C.Species: Homo sapiens (man)
C.Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C.Accession: A54740
R.Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A.Title: An interleukin-4-induced transcription factor: IL-4 stat.
A.Reference number: A54740; MUID:94367369; PMID:8085155
A.Accession: A54740
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-848 <HOU>
A.Cross-references: UNIPROT:P42226
C.Superfamily: human signal transducer and transcription activator STAT5A
C.Keywords: DNA binding; transcription regulation

Query Match      11.4%; Score 91.5; DB 2; Length 848;
Best Local Similarity 21.7%; Pred. No. 3.7;
Matches          43; Conservative 25; Mismatches 69; Indels 61; Gaps 8

QY   1 MAQNQLQOLDTRYLKQHLYSDTFPPELROFLAPWIESODWAAYAAKESHATLVFHNLL 60
     : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db   1 MSLWGVLGKMPP-----EKVORLYVD-FPHLRHLGLDWLESPQWEILVGSDAFCCNLASAL 56
     : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

QY   61 LGEIDQ-----QYSRFLESNNVL---YQHN----LRRIKFLOS-----RY 94
     : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db   57 LSDTVQHLQA SVGEQEGSTII QHTLSIESIQRPDLKL VATFRLOLGKKAVMEQFRH 116
     : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY   95 LEKPMEIARI VARCWESRL-----IQTATAAQGGGANHP 132
     : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db   117 LFMPFH-----WKQEIKFKTGLRRLRHQRVGEIHLLREALQGAEAGVSLHSLTIE 167

```

```
QY 133 TAAVVTKEQKQMLEQHLQD 150
Db 168 TPANGTGPSEALAMLQOE 185

RESULT 13
T22552
hypothetical protein ZK1151.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T22552; T27703
R:Harris, B.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19580
A:Accession: T22552
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1355 <WIL>
A:Cross-references: EMBL:Z92788; PIDN:CA807214.1; GSPDB:GN00019; CESP:ZK1151.1
A:Experimental source: clone F53B8
R:Harris, B.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20408
A:Accession: T27703
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1355 <W12>
A:Cross-references: EMBL:Z93398; PIDN:CA807724.1; GSPDB:GN00019; CESP:ZK1151.1
A:Experimental source: clone ZK1151
C:Genetics:
A:Gene: CESP:ZK1151.1
A:Map position: 1
A:Introns: 94/3; 124/3; 150/3; 209/3; 248/3; 311/3; 424/3; 734/2; 934/2; 1104/3; 1167/3;

Query Match 11.0%; Score 88; DB 2; Length 1355;
Best Local Similarity 25.3%; Pred. No. 13;
Matches 44; Conservative 25; Mismatches 57; Indels 42; Gaps 10;

QY 4 WNOQLQDLD---TRYLKQ-LHQL-----YSD-----TFPMELQFLA 35
Db 677 WSDIKQLDPLMTNYKQLLHEMELREKQYNDVHNGAALLNQGHPAIRVIEVYLRQMS 736

QY 36 PWIESQDWAYAASK--ESHA--TLVFHNLGEIDQOYSRFLQESNVLYQHNLRIKQFLQ 91
Db 737 QW-----DWLLALSCLBEHLRDALNLKSFMEASDA-EAWTQESVRLNNYNTDFSL 791

QY 92 --SRYLEKPMETARIVARCLWEESRLQTAATA--QOQGOANHP 132
Db 792 EGERFLRELDEIKELNKYHQVLMALTEKASISPLWQGRGRIHPH 837

RESULT 14
T40287
hypothetical protein SPBC354.07c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40287
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21918
A:Accession: T40287
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-371 <WOO>
A:Cross-references: EMBL:AL022071; PIDN:CAA17807.1; GSPDB:GN00067; SPDB:SPBC354.07c
A:Experimental source: strain 972h-; cosmid c354
C:Genetics:
A:Gene: SPDB:SPBC354.07c
A:Map position: 2
A:Introns: 8/2; 75/3

Query Match 10.3%; Score 82.5; DB 2; Length 371;
Best Local Similarity 24.0%; Pred. No. 8.4;
```

```
Matches 44; Conservative 31; Mismatches 57; Indels 51; Gaps 9;
QY 5 NOLQQLDTRYLKQHLQYSDTFP---MELRQFLAPWIESQDWAYAASKESHATLVFHNLL 61
Db 147 NQLQLRV-HLEKYNETYITLPNISLEGWFWAPYIELYGSTIVSVNTVITKIDYSGR 205

QY 62 GEIDQOYSRFLQES--NVLYQHN-----LRRIKQFLQSRYLE-- 96
Db 206 G-----YFRGTQKNSFKATIFEKNEPDYIIEGVWGTGSKLTIPSLKSTIFPLSPLEAT 260

QY 97 ---KP-METARIVARCLWEESRLQTAATAAQGGQANHPATAAVVTEKQOQMLRQHLQDV 151
Db 261 PITVKPESEMGDWESRNWKE-----VSAALASGNVD-----IVSKKSTIEQSQRDM 308

QY 152 RXR 154
Db 309 RKK 311

RESULT 15
F71884
probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: F71884
R:Alim, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397; 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path-
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: F71884
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-373 <ARN>
A:Cross-references: UNIPROT:Q9ZK44; GB:AE001511; GB:AE001439; NID:g4155382; PIDN:RAD0639
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0820

Query Match 10.3%; Score 82.5; DB 2; Length 373;
Best Local Similarity 33.8%; Pred. No. 8.4;
Matches 27; Conservative 14; Mismatches 26; Indels 13; Gaps 5;

QY 18 LHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNV 77
Db 287 LH-FYADEKFW--KHFGYPY--SKEWHQVAFKTSFESLVFENLVGKIE---TFTE---- 333

QY 78 LYQHNLRRIRIKQFLQSRYLEK 97
Db 334 LNDHNKKSFPFELNRLNKK 353

Search completed: May 5, 2005, 15:01:50
Job time : 18.2329 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 14:55:35 ; Search time 41.6706 Seconds
(without alignments)

1892.467 Million cell updates/sec

Title: US-10-090-185-8

Perfect score: 800

Sequence: 1 MAQWNQLQDLTRYLKQLHQ.....AVVTEKQOMLEQLQDVQRK 154

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792	99.0	770	1 STA3 HUMAN	P40763 homo sapien
2	792	99.0	770	1 STA3 MOUSE	P42227 mus musculus
3	792	99.0	770	1 STA3 RAT	P52631 rattus norv
4	786	98.2	770	1 STA3 BOVIN	P61635 bos taurus
5	779	97.4	771	2 Q6DV79	Q6dv79 gallus gall
6	760	95.0	769	2 Q9PVX8	Q9pvx8 xenopus lae
7	749	93.6	766	2 Q7ZXX3	Q7zxx3 xenopus lae
8	694.5	86.8	414	2 Q7ZTS5	Q7zts5 brachydanio
9	694.5	86.8	786	2 Q6NV46	Q6nv46 brachydanio
10	694.5	86.8	806	2 Q93599	Q93599 brachydanio
11	691.5	86.4	767	2 O13133	O13133 oncorhynch
12	685.5	85.7	765	2 Q6DV73	Q6dv73 oryzias lat
13	685.5	85.7	785	2 Q6GV87	Q6gv87 oryzias lat
14	681.5	85.2	764	2 Q90Y16	Q90y16 tetraodon f
15	401	50.1	751	2 Q8JGNO	Q8jgn0 xenopus lae
16	380	47.5	750	1 STA1 HUMAN	P42224 homo sapien
17	380	47.5	750	2 Q68D00	Q68d00 homo sapien
18	379	47.4	712	2 Q6P6Q7	Q6p6q7 rattus norv
19	379	47.4	1165	2 Q7TP57	Q7tp57 rattus norv
20	378	47.2	712	2 Q99K94	Q99k94 mus musculus
21	378	47.2	749	1 STA1 MOUSE	P42225 mus musculus
22	378	47.2	749	2 Q8C3V4	Q8c3v4 mus musculus
23	378	47.2	749	2 Q8C497	Q8c497 mus musculus
24	378	47.2	749	2 Q9D323	Q9d323 mus musculus
25	378	47.2	749	2 Q9QXK0	Q9qxk0 rattus norv
26	378	47.2	755	2 Q8C8M3	Q8c8m3 mus musculus
27	378	47.2	757	2 Q764W5	Q764w5 sus scrofa
28	374.5	44.3	758	2 Q90Y17	Q90y17 tetraodon f
29	351	43.9	754	2 O13132	O13132 oncorhynch
30	346	43.2	754	2 O13131	O13131 oncorhynch
31	336.5	42.1	718	2 Q801Y2	Q801y2 carassius a

RESULT 1

ID	STA3 HUMAN	STANDARD;	PRT;	770 AA.
AC	P40763: O14916; Q9BW54;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Signal transducer and activator of transcription 3 (Acute-phase response factor).			
DE	Name=STAT3; Synonyms=APRF;			
GN	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
LN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;			
RA	AKira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.;			
RT	"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling pathway.";			
RT	Cell 77:63-71 (1994).			
LN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;			
RA	Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;			
RT	"Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence.";			
LN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILB-143.			
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O., Rajkumar N., Yi Q., Nickerson D.A.;			
RT	"SeattlesNPs. NHLBI HUG6682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
LN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).			
RC	TISSUE=Kidney, and Pancreas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Collins F.E., Wagner L., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Romanov S.P., Casavant T.L., Scheetz T.E., Brownstein M., Sorescu M.B., Tashy S., Carninci P., Prange C., Brownstein M.J., Ustin T.B., Toshiyuki S., Abramson R.D., Mullany S.H., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
[5]
RN SEQUENCE OF 564-704 FROM N.A.
RP TISSUE=Liver;
RC Della Pietra L., Bressan A., Perzotti A.R., Serlupi-Crescenzi O.,
RA Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
[6]
RN PHOSPHORYLATION ON SERINE.
RX MEDLINE=95215843; Pubmed=7701321;
RA Zhang X., Bilen J., Li H.-C., Schindler C., Chen-Kiang S.;
RT "Requirement of serine phosphorylation for formation of STAT-promoter
complexes.",
RL Science 267:1990-1994(1995).
[7]
RN INTERACTION WITH NCOAL.
RX Pubmed=11773079; DOI=10.1074/jbc.M11486200;
RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.,
RT coactivator NcoA/SRC1a.",
RL J. Biol. Chem. 277:8004-8011(2002).
CC -I- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
acute-phase protein genes.
CC -I- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -I- SUBUNIT: Forms a homodimer or a heterodimer with a related family
member (at least STAT1). Interacts with NCOAL.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
in response to phosphorylation.
CC -I- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P40763-1; Sequence=VSP_010474;
CC Name=Del-701;
CC IsoId=P40763-2; Sequence=VSP_010474;
CC -I- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
muscle, kidney and pancreas.
CC -I- PM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
ILF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
is important for the formation of stable DNA-binding STAT3
homodimers and maximal transcriptional activity.
CC -I- SIMILARITY: Belongs to the transcription factor STAT family.
CC -I- SIMILARITY: Contains 1 SH2 domain.
CC
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; L29277; AAA58374.1; -;
CC EMBL; AJ012463; CAAL0032.1; -;
CC EMBL; AY572796; AAS66986.1; -;
CC EMBL; BC000627; AAH00627.1; -;
CC EMBL; BC014482; AAH14482.1; -;
CC EMBL; AF029311; AAB84254.1; -;
CC PIR; A54444; A54444.
CC HSP; P42227; IBL1.
CC TRANSFAC; T01493; -;
CC Genew; HGNC:11364; STAT3.
CC H-InVDB; HIX0013840; -;
CC MIM; 102582; -;
CC GO; GO:0005737; Cytoplasm; TAS.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0005062; C:hematopoietin/interferon-class (D200-domain. . .; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS0001; SH2; 1.
KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
FT VARSPLIC 701 701 Missing (in isoform Del-701).
FT VARIANT 32 32 Q -> K (in dbSNP:1803125).
FT VARIANT 143 143 /FTId=VAR_018683.
FT CONFLICT 288 288 /FTId=VAR_018679.
FT CONFLICT 460 460 Q -> H (in Ref. 1).
FT CONFLICT 548 548 P -> S (in Ref. 1).
FT CONFLICT 561 561 K -> N (in Ref. 1).
FT CONFLICT 667 667 F -> Y (in Ref. 1).
FT CONFLICT 730 730 V -> L (in Ref. 1).
FT CONFLICT 770 770 T -> A (in Ref. 1).
SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
Query Match 99.0%; Score 792; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 7 3e-60;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQWNLQQLDTRYLKHLYSDTTPFMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
DB 1 MAQWNLQQLDTRYLKHLYSDTTPFMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
QY 61 LGSDIQQYSRFLQESNVLYOHNLRRIKQFLOSYLEKPMELRIARIVARCLWEESRLQTAA 120
DB 61 LGSDIQQYSRFLQESNVLYOHNLRRIKQFLOSYLEKPMELRIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQGANHPAAVVTKEQKQMLEQHLQDVRRK 154
DB 121 TAAQGGQGANHPAAVVTKEQKQMLEQHLQDVRRK 154
RESULT 2
STA3_MOUSE
ID STA3_MOUSE STANDARD; PRT; 770 AA.
AC P42227;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
response factor).
DE Names=Stat3; Synonyms=Aprf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
AND 632-640.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94208062; Pubmed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gp130-mediated signaling

RT pathway.";
Cell 77:63-71(1994).
[2]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RP TISSUE=Thymus;
RX MEDLINE=94188718; PubMed=8140422;
RA Zhong Z., Wen Z., Darnell J.E. Jr.;
RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
response to epidermal growth factor and interleukin-6.";
RL Science 264:95-98(1994).
[3]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RP TISSUE=Brain;
RX MEDLINE=95014185; PubMed=7523373;
RA Raz R., Durbin J.E., Levy D.E.;
RT "Acute phase response factor and additional members of the interferon-
stimulated gene factor 3 family integrate diverse signals from
cytokines, interferons, and growth factors.";
RL J. Biol. Chem. 269:24391-24395(1994).
[4]
RN SEQUENCE FROM N.A. (ISOFORM STAT3B).
RP STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
RX MEDLINE=96016116; PubMed=7568080;
RA Schaefer T.S., Sanders L.K., Nathans D.;
RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
form of Stat3.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
[5]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RP STRAIN=129/SVJ;
RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
RA Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zen L., Oka T.,
Dewar K., Hennighausen L.;
RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
zebrafish to mouse.";
RL Genomics 71:150-155(2001).
[6]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RP STRAIN=C57BL/6J, and NOD/LtJ;
RA Davoodi-Semirami A., She J.-X.;
RT "A mutant Stat5b with weaker DNA binding defines a key defective
pathway in non-obese diabetic (NOD) mice.";
RL Submitted (MAY-2003) to the ENBL/GenBank/DBJ databases.
[7]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RP STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
RN PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.
RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
RA Wen Z., Zhong Z., Darnell J.E. Jr.;
RT "Maximal activation of transcription by Stat1 and Stat3 requires both
tyrosine and serine phosphorylation."

Cell 82:241-250(1995).
[9]
RN X-RAY CRYSTALLOGRAPHY (2.25 ÅNGSTRÖMS) OF 136-716.
RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
RA Becker S., Groner B., Mueller C.W.;
RT "Three-dimensional structure of the Stat3beta homodimer bound to
DNA.";
RL Nature 394:145-151(1998).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
acute-phase protein genes. STAT3B interacts with the N-terminal
part of JUN to activate such promoters in a cooperative way.
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
member (at least STAT1). Interacts with NCOAL (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
in response to phosphorylation.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=Stat3A;
IsoId=P42227-1; Sequence=Displayed;
Name=Stat3B;
IsoId=P42227-2; Sequence=VSP_006287;
Name=Del-701;
IsoId=P42227-3; Sequence=VSP_010475;
CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
kidney. STAT3B is also detected in the liver, although in a much
less abundant manner.
CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
is important for the formation of stable DNA-binding STAT3
homodimers and maximal transcriptional activity (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.

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or send an email to license@isb-sib.ch).

DR EMBL; L29278; AAA37254.1; -;
DR EMBL; U06922; AAA19452.1; -;
DR EMBL; U08378; AAA56668.1; -;
DR EMBL; U30709; AAC52612.1; -;
DR EMBL; AF246978; AAL59017.1; -;
DR EMBL; AY299489; AAQ75418.1; -;
DR EMBL; AY299490; AAQ75419.1; -;
DR EMBL; BC003806; AAH03806.1; -;
DR PIR; I49508; I49508.
DR PDB; 1BG1; X-ray; A=1-722.
DR TRANSFAC; T01574; -;
DR MGD; MGI:103038; Stat3.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0003677; F:DNA binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0015663; F:transcriptional activator activity; IDA.
DR GO; GO:0007259; P:JAK-STAT cascade; IDA.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
DR InterPro; IPR008967; P53 like DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
KW 3D-structure; Activator; Acute phase; Alternative splicing;
Direct protein sequencing; DNA-binding; Nuclear protein;

Phosphorylation; SH2 domain; Transcription regulation.
 KW DOMAIN 580 670 SH2.
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT MOD_RES 727 727 Phosphoserine.
 FT VARSPPLIC 716 770 TTCSNTIDLPMSPTSLDLMQFGNGEGAPSPAGGQFESLT
 FT FDMDLTSECATSPM -> FIDAVWK (in isoform
 FT Stat3B).
 FT /FTid=VSP_006287.
 FT Missing (in isoform Del-701).
 FT /FTid=VSP_010475.
 FT S-A: Decreased transcriptional
 FT activation.
 FT MUTAGEN 727 727 E -> K (in Ref. 2).
 FT S -> T (in Ref. 2 and 4).
 FT M -> I (in Ref. 1).
 FT
 FT VARSPPLIC 701 701
 FT
 FT MUTAGEN 727 727
 FT
 FT CONFLICT 16 16
 FT CONFLICT 25 25
 FT CONFLICT 394 394
 FT HELIX 139 180
 FT TURN 181 182
 FT TURN 197 198
 FT HELIX 238 238
 FT TURN 239 251
 FT HELIX 252 253
 FT TURN 261 290
 FT HELIX 294 295
 FT TURN 297 301
 FT TURN 302 320
 FT STRAND 321 328
 FT TURN 330 331
 FT TURN 333 334
 FT TURN 336 337
 FT STRAND 338 340
 FT TURN 341 342
 FT STRAND 345 351

Query Match 99.0%; Score 792; DB 1; Length 770;
 Best Local Similarity 98.7%; Pred. No. 7.3e-60;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
 DB 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLQATA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLQATA 120
 QY 121 TAAQCGQGANHPHTAAVVTKEQKMLEQHLQDVRRK 154
 DB 121 TAAQCGQGANHPHTAAVVTKEQKMLEQHLQDVRRK 154

RESULT 3
 ID_STA3_RAT STANDARD; PRT; 770 AA.
 AC P52631;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3.
 GN Name=Stat3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.23998;
 RA Ripberger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
 RA Fey G.H.;
 RT "Transcription factors Stat3 and Stat5b are present in rat liver
 RT nuclei late in an acute phase response and bind interleukin-6 response
 RT elements.";

J. Biol. Chem. 270:29998-30006(1995).
 RL J. Biol. Chem. 270:29998-30006(1995).
 CC -I- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes.
 CC -I- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -I- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOA1 (By similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation (By similarity).
 CC -I- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity (By similarity).
 CC -I- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -I- SIMILARITY: Contains 1 SH2 domain.
 CC
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 CC
 CC EMBL; X91810; CAAG2920.1; -.
 CC DR HSSP; P42227; 1BG1.
 CC DR RGD; 3772; Stat3.
 CC DR InterPro; IPR008967; P53_like_DNA_bnd.
 CC DR InterPro; IPR009980; SH2.
 CC DR InterPro; IPR01217; STAT.
 CC DR Pfam; PF00017; SH2; 1.
 CC DR Pfam; PF01017; STAT_alpha; 1.
 CC DR Pfam; PF02864; STAT_bind; 1.
 CC DR Pfam; PF02865; STAT_int; 1.
 CC DR SMART; SM00252; SH2; 1.
 CC DR PROSITE; PS00001; SH2; 1.
 CC KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
 CC Transcription regulation.
 FT DOMAIN 580 670 SH2.
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT MOD_RES 727 727 Phosphoserine (By similarity).
 SQ SEQUENCE 770 AA; 89309 MM; D74A0C76954754ED CRC64;
 Query Match 99.0%; Score 792; DB 1; Length 770;
 Best Local Similarity 98.7%; Pred. No. 7.3e-60;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
 DB 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLQATA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLQATA 120
 QY 121 TAAQCGQGANHPHTAAVVTKEQKMLEQHLQDVRRK 154
 DB 121 TAAQCGQGANHPHTAAVVTKEQKMLEQHLQDVRRK 154

RESULT 4
 ID_STA3_BOVIN STANDARD; PRT; 770 AA.
 AC P61635;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3.
 GN Name=Stat3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.


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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RT "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
RL during ruminant evolution.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes (By similarity).
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation (By similarity).
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ620655; CAF06182.1; -.
DR PROSITE; PS50001; SH2; 1.
KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73E83274 CRC64;

Query Match 98.2%; Score 786; DB 1; Length 770;
Best Local Similarity 98.1%; Pred. No. 2.4e-59;
Matches 151; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHOLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQLHOLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQANHPTAAVTEKQOMLEQHLQDVYRKR 154
DB 121 TAAQGGQANHPTAAVTEKQOMLEQHLQDVYRKR 154

RESULT 5
Q6DV79 PRELIMINARY; PRT; 771 AA.
AC Q6DV79;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Signal transducer and activator of transcription 3.
OS Gallus gallus (Chicken).
OC Archosauria; Aves; Neognathae; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641397; AAT64887.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.

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DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match 97.4%; Score 779; DB 2; Length 771;
Best Local Similarity 96.8%; Pred. No. 9.7e-59;
Matches 149; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHOLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQLHOLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQANHPTAAVTEKQOMLEQHLQDVYRKR 154
DB 121 TAAQGGQANHPTAAVTEKQOMLEQHLQDVYRKR 154

RESULT 6
Q9PVX8 PRELIMINARY; PRT; 769 AA.
AC Q9PVX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat 3.
GN Name=stat 3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
RA Asashima M., Yokota T.;
RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
RT embryos independent of BMP-4.";
RL Dev. Biol. 216:481-490(1999).
DR EMBL; AB017701; BAA86061.1; -.
DR HSSP; P42227; IBGL.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SMO0252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;

Query Match 95.0%; Score 760; DB 2; Length 769;
Best Local Similarity 94.2%; Pred. No. 4.2e-57;
Matches 145; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVPHNL 60
Db 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVPHNL 60
QY 61 LGEIDQOYSRFLQESNVLYOHNLRRRIKQFLQSRYLEKPMIARIVARCLWEESRLQTA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRRRIKQFLQSRYLEKPMIARIVARCLWEESRLQTA 120
QY 121 TAAQGGQGANHPAAVTEKQMLQHLQDVRRK 154
Db 121 TAAQGGQGANHPAAVTEKQMLQHLQDVRRK 154

RESULT 7
Q7ZXK3 PRELIMINARY; PRT; 766 AA.
ID Q7ZXK3
AC Q7ZXK3
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE Stat3-A protein.
GN Name-stat3-A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044717; AHA44717.1; -.
DR HSSP; P42227; IBGI.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

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DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;

Query Match 93.6%; Score 749; DB 2; Length 766;
Best Local Similarity 92.2%; Pred. No. 3.7e-56;
Matches 142; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVPHNL 60
Db 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVPHNL 60
QY 61 LGEIDQOYSRFLQESNVLYOHNLRRRIKQFLQSRYLEKPMIARIVARCLWEESRLQTA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRRRIKQFLQSRYLEKPMIARIVARCLWEESRLQTA 120
QY 121 TAAQGGQGANHPAAVTEKQMLQHLQDVRRK 154
Db 121 TAAQGGQGANHPAAVTEKQMLQHLQDVRRK 154

RESULT 8
Q7ZTS5 PRELIMINARY; PRT; 414 AA.
ID Q7ZTS5
AC Q7ZTS5
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Stat3 protein.
GN Name-stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045276; AAH45276.1; -.
DR HSSP; P42227; IBGI.

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DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 414 AA; 49253 MW; 0FFD1B509B7526BD CRC64;

Query Match      86.8%; Score 694.5; DB 2; Length 414;
Best Local Similarity 86.4%; Pred. No. 9.3e-52;
Matches 133; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTA 120

QY 121 TAAQGGQQAHPHTAAVTEKQMLEQHLQDVRKR 154
DB 120 TTAQDQGVAAHTGTVTTEKQMLEHNLQDIRKR 153

RESULT 9
Q6NV46 PRELIMINARY; PRT; 786 AA.
ID Q6NV46
AC Q6NV46
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stat3 protein.
GN Names:stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Kettum M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 414 AA; 49253 MW; 0FFD1B509B7526BD CRC64;

Query Match      86.8%; Score 694.5; DB 2; Length 786;
Best Local Similarity 86.4%; Pred. No. 2e-51;
Matches 133; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTA 120

QY 121 TAAQGGQQAHPHTAAVTEKQMLEQHLQDVRKR 154
DB 120 TTAQDQGVAAHTGTVTTEKQMLEHNLQDIRKR 153

RESULT 10
O93599 PRELIMINARY; PRT; 806 AA.
ID O93599
AC O93599;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Names:stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oates A.C.;
RL Thesis (1998), University of Melbourne, Australia.
DR EMBL; AJ005593; CAA06677.1; -.
DR HSSP; P42227; IBLI.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007165; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match      86.8%; Score 694.5; DB 2; Length 806;
Best Local Similarity 86.4%; Pred. No. 2e-51;
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Matches 133; Conservative 10; Mismatches 10; Indels 1; Gaps 1;
QY 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
DB 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
QY 61 LGEIDQYSRFLQENNVLYQHNLRRIKQFLQSKYLEKPMIARIVARCLWEESRLQTA 120
DB 61 LGEIDQYSRFLQENNVLYQHNLRRIKQFLQSKYLEKPMIARIVARCLWEESRLQTA 119
QY 121 TAAQGGQGANHTAAVTEKQMLEQHLQDVRKR 154
DB 120 TTAQDQGVAAHTPGTVVTEKQMLEHNLQDIRKR 153
RESULT 11
ID O13133 PRELIMINARY; PRT; 767 AA.
AC O13133;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Stat3.
GN Name=rbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RA SEQUENCE FROM N.A.
RP Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AB60926.1; -
DR HSP; P42227; IBI.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;
Query Match 86.4%; Score 691.5; DB 2; Length 767;
Best Local Similarity 85.7%; Pred. No. 3.4e-51;
Matches 133; Conservative 12; Mismatches 9; Indels 1; Gaps 1;
QY 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
DB 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
QY 61 LGEIDQYSRFLQENNVLYQHNLRRIKQFLQSKYLEKPMIARIVARCLWEESRLQTA 120
DB 61 LGEIDQYSRFLQENNVLYQHNLRRIKQFLQSKYLEKPMIARIVARCLWEESRLQTA 120
QY 121 TAAQGGQGANHTAAVTEKQMLEQHLQDVRKR 154
DB 120 TTAQDQGVAAHTPGTVVTEKQMLEHNLQDIRKR 153
RESULT 12
ID Q6DV3 PRELIMINARY; PRT; 765 AA.
AC Q6DV3;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
```

```
DE Signal transducer and activation of transcription factor 3.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Beloniformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RA SEQUENCE FROM N.A.
RP Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT64912.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PSS0001; SH2; 1.
SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;
Query Match 85.7%; Score 685.5; DB 2; Length 765;
Best Local Similarity 85.1%; Pred. No. 1.1e-50;
Matches 131; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
QY 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
DB 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHN 60
QY 61 LGEIDQYSRFLQENNVLYQHNLRRIKQFLQSKYLEKPMIARIVARCLWEESRLQTA 120
DB 61 LGEIDQYSRFLQENNVLYQHNLRRIKQFLQSKYLEKPMIARIVARCLWEESRLQTA 119
QY 121 TAAQGGQGANHTAAVTEKQMLEQHLQDVRKR 154
DB 120 TTSQDQGSAAHTPGTVVTEKQMLEHNLQDIRKR 153
RESULT 13
ID Q6GUE7 PRELIMINARY; PRT; 785 AA.
AC Q6GUE7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Signal transducer and activator of transcription 3 isoform 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Beloniformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RA SEQUENCE FROM N.A.
RP Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT64364.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
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DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;

Query Match      85.7%; Score 685.5; DB 2; Length 785;
Best Local Similarity 85.1%; Pred. No. 1.2e-50;
Matches 131; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MAQWNLQQLDTRYLEQLYHLYSDSPFMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 LGEIDQOYSRFLQSNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LGEIDQOYSRFLQSNVLYQHNLRIKQHLQSKYLEKPMETARIVARCLWEESRLLOT-A 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 TAAQGGQGANHPTAAVTEKQOMLEQHLQDVVRK 154
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 TSTSQDGSAAHPTGVVTEKQOILEHNLQDIRK 153
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STAT3
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Liu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSP; P42227; IBL1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFE18BEFD8BE CRC64;

Query Match      85.2%; Score 681.5; DB 2; Length 764;
Best Local Similarity 85.7%; Pred. No. 2.5e-50;
Matches 132; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MAQWNLQQLDTRYLEQLYHLYSDSPFMELRQFLAPWIESQDWAYAAKESHATLVSHNL 60
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Qy 61 LGEIDQOYSRFLQSNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
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Db 61 LGEIDQOYSRFLQSNVLYQHNLRIKQHLQSKYLEKPMETARIVARCLWEESRLLOTAS 120
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Qy 121 TAAQGGQGANHPTAAVTEKQOMLEQHLQDVVRK 154
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Db 121 TVAQD-GQANPSTGVVTEKQOMLELNLQDIRK 153
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RESULT 15

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Q8JGNO PRELIMINARY; PRT; 751 AA.
AC Q8JGNO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Statl.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21098508; PubMed=1164887; DOI=10.1016/S0145-305X(00)00050-1;
RA Turpen J.B., Carlson D.L., Huang C.;
RT "Cloning and developmental expression of Xenopus Statl.";
RL Dev. Comp. Immunol. 25:219-229(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Turpen J.B., Carlson D.L., Huang C.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101602; AAM51552.1; -.
DR HSP; P42224; IBL5.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 751 AA; 86497 MW; 788810A08B0889EA CRC64;

Query Match      50.1%; Score 401; DB 2; Length 751;
Best Local Similarity 48.7%; Pred. No. 4e-26;
Matches 75; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

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Db 1 MAQWYDLQIDTRYLEQVHQLYDSDSPFMELRQFLAPWLEQDWEHAANNYSVATILFHGL 60
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Qy 61 LGEIDQOYSRFLQSNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
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Db 61 LSQLDQOYSRFLQSNVLYQHNLRIKSKRNQLQDHQFQEDPVQVQMIINNCLREESKILCNA- 119
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Qy 121 TAAQGGQGANHPTAAVTEKQOMLEQHLQDVVRK 154
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Db 120 -RASNNQVGSQTOTVMLDKQKELDKKVDVRNR 152
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Search completed: May 5, 2005, 14:57:40
Job time : 43.6706 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2005, 14:59:00 ; Search time 114.139 Seconds
(without alignments)
792.064 Million cell updates/sec

Title: US-10-090-185-9
Perfect score: 1388
Sequence: 1 RCWESRLLOTATAAQQG.....LNVLKIKVICDKSDGVAA 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0
Maximum Match 100%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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17:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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19:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1388	100.0	271	13	US-10-090-185-9
2	1388	100.0	770	11	US-09-876-773-12
3	1388	100.0	770	17	US-10-639-617-12
4	1377	99.2	720	15	US-10-380-020-4
5	1377	99.2	769	15	US-10-380-020-2
6	1377	99.2	769	15	US-10-380-020-5
7	1377	99.2	770	14	US-10-045-792-8
8	1377	99.2	770	14	US-10-038-010-56
9	1377	99.2	770	14	US-10-117-087-2
10	1377	99.2	793	9	US-09-925-302-780
11	1377	99.2	793	10	US-09-925-302-780
12	1374	99.0	770	15	US-10-116-275-329
13	1372	98.8	770	15	US-10-116-275-349

14	1290	92.9	252	13	US-10-090-185-14	Sequence 14, Appl
15	1212	87.3	236	13	US-10-090-185-15	Sequence 15, Appl
16	1172	84.4	229	13	US-10-090-185-18	Sequence 18, Appl
17	1172	84.4	229	13	US-10-090-185-28	Sequence 28, Appl
18	1168	84.1	229	13	US-10-090-185-31	Sequence 31, Appl
19	1167	84.1	229	13	US-10-090-185-30	Sequence 30, Appl
20	1155	83.2	229	13	US-10-090-185-29	Sequence 29, Appl
21	1142	82.3	223	13	US-10-090-185-22	Sequence 22, Appl
22	1094	78.8	213	13	US-10-090-185-19	Sequence 19, Appl
23	943	67.9	185	13	US-10-090-185-23	Sequence 23, Appl
24	899	64.8	176	13	US-10-090-185-16	Sequence 16, Appl
25	723	52.1	143	13	US-10-090-185-17	Sequence 17, Appl
26	669	48.2	129	13	US-10-090-185-24	Sequence 24, Appl
27	654	47.1	749	9	US-09-833-205-4	Sequence 4, Appl
28	653	47.0	128	13	US-10-090-185-20	Sequence 20, Appl
29	647	46.6	268	13	US-10-090-185-12	Sequence 12, Appl
30	647	46.6	712	11	US-09-876-773-6	Sequence 6, Appl
31	647	46.6	712	14	US-10-245-120-2	Sequence 2, Appl
32	647	46.6	712	17	US-10-639-617-6	Sequence 6, Appl
33	647	46.6	712	17	US-10-936-390-5	Sequence 5, Appl
34	647	46.6	750	9	US-09-833-205-2	Sequence 2, Appl
35	647	46.6	750	11	US-09-876-773-4	Sequence 4, Appl
36	647	46.6	750	14	US-10-245-120-1	Sequence 1, Appl
37	647	46.6	750	14	US-10-308-279-44	Sequence 44, Appl
38	647	46.6	750	16	US-10-755-889-352	Sequence 352, App
39	647	46.6	750	16	US-10-755-889-823	Sequence 823, App
40	647	46.6	750	17	US-10-492-043-19	Sequence 19, Appl
41	647	46.6	750	17	US-10-639-617-4	Sequence 4, Appl
42	647	46.6	786	9	US-09-925-297-550	Sequence 550, App
43	623	44.9	582	14	US-10-245-120-3	Sequence 3, Appl
44	619	44.6	749	9	US-09-833-205-6	Sequence 6, Appl
45	619	44.6	749	11	US-09-876-773-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-10-090-185-9
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR E
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-090-185-9

Query Match 100.0%; Score 1388; DB 13; Length 271;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	RCWESRLLOTATAAQQGQGHHPHTAAVTEKQMLQHLQDVRRKVDLEQKMKVVE	60
Db	1	RCWESRLLOTATAAQQGQGHHPHTAAVTEKQMLQHLQDVRRKVDLEQKMKVVE	60
Qy	61	NLODDFDNFYKTLKSGQDMQDLGNNGSVTRQKMQLEQMLTALDOMRRSIVSELAGLLS	120
Db	61	NLODDFDNFYKTLKSGQDMQDLGNNGSVTRQKMQLEQMLTALDOMRRSIVSELAGLLS	120

QY 121 AMEYVOKLTDEELADWKRPEIACIGGPNICLDRLNNWITSLAESQLQTRQOIKKLEE 180
DB 121 AMEYVOKLTDEELADWKRPEIACIGGPNICLDRLNNWITSLAESQLQTRQOIKKLEE 180
QY 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKTGVQFT 240
DB 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKTGVQFT 240
QY 241 TKVRLLVKFPPELNYQLKIKVICDKDGDVAA 271
DB 241 TKVRLLVKFPPELNYQLKIKVICDKDGDVAA 271

RESULT 2

US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040059318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Fu, Xian-Yuan
; Schindler, Christian W.
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 100.0%; Score 1388; DB 11; Length 770;
Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCLWEESRLLOTAATAAQGGQANHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQGGQANHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 166
QY 61 NLQDDPFDNFYKTLKSGQDMODLNGNNSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLS 120
DB 167 NLQDDPFDNFYKTLKSGQDMODLNGNNSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLS 226
QY 121 AMEYVOKLTDEELADWKRPEIACIGGPNICLDRLNNWITSLAESQLQTRQOIKKLEE 180
DB 227 AMEYVOKLTDEELADWKRPEIACIGGPNICLDRLNNWITSLAESQLQTRQOIKKLEE 286
QY 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKTGVQFT 240
DB 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVICDKDGDVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVICDKDGDVAA 377

RESULT 3

US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Fu, Xian-Yuan
; Schindler, Christian W.
; Wen, Zilong
; Zhong, Zhong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids


```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match      100.0%; Score 1388; DB 17; Length 770;
Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQGGQANHTAAVVTKEQKQMLEQHLQDVRRKRVODLEQKMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHTAAVVTKEQKQMLEQHLQDVRRKRVODLEQKMKVVE 166

Qy 61 NLQDDFDNFYKTLKSQGDMDLNGNOSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDFDNFYKTLKSQGDMDLNGNOSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNWITSLSAESQLOTRQOIKLEE 180
Db 227 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNWITSLSAESQLOTRQOIKLEE 286

Qy 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTVQFT 240
Db 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 377

RESULT 4
US-10-380-020-4
; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match      99.2%; Score 1377; DB 15; Length 769;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQGGQANHTAAVVTKEQKQMLEQHLQDVRRKRVODLEQKMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHTAAVVTKEQKQMLEQHLQDVRRKRVODLEQKMKVVE 166

Qy 61 NLQDDFDNFYKTLKSQGDMDLNGNOSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDFDNFYKTLKSQGDMDLNGNOSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNWITSLSAESQLOTRQOIKLEE 180
Db 227 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNWITSLSAESQLOTRQOIKLEE 286

Qy 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTVQFT 240
Db 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 377

RESULT 5
US-10-380-020-2
; Sequence 2, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT<
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match      99.2%; Score 1377; DB 15; Length 769;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQGGQANHTAAVVTKEQKQMLEQHLQDVRRKRVODLEQKMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHTAAVVTKEQKQMLEQHLQDVRRKRVODLEQKMKVVE 166

Qy 61 NLQDDFDNFYKTLKSQGDMDLNGNOSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDFDNFYKTLKSQGDMDLNGNOSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNWITSLSAESQLOTRQOIKLEE 180
Db 227 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNWITSLSAESQLOTRQOIKLEE 286

Qy 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTVQFT 240
Db 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 377

RESULT 6
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 769
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match 99.2%; Score 1377; DB 15; Length 769;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCLWEESRLLOTAATAAQAQGGQANHPHTAAVTEKQOQMLEOHLQDVVKRVQDLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQAQGGQANHPHTAAVTEKQOQMLEOHLQDVVKRVQDLEQKMKVVE 166
QY 61 NLQDDDFNFKTLKSGQDMQDLNGNNSVTRQKQOQMLEOHLQDVVKRVQDLEQKMKVVE 120
DB 167 NLQDDDFNFKTLKSGQDMQDLNGNNSVTRQKQOQMLEOHLQDVVKRVQDLEQKMKVVE 226
QY 121 AMEYVQKTLTDEBLADWKRPEIACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180
DB 227 AMEYVQKTLTDEBLADWKRPEIACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 286
QY 181 LOOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFT 240
DB 287 LOOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 7
US-10-045-792-8
; Sequence 8, Application US/10045792
; Publication No. US20030003563A1
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; Moarefi, Ismail
; Darnell, Jr., James E.
; Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5900
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
;

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8

Query Match 99.2%; Score 1377; DB 14; Length 770;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCLWEESRLLOTAATAAQAQGGQANHPHTAAVTEKQOQMLEOHLQDVVKRVQDLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQAQGGQANHPHTAAVTEKQOQMLEOHLQDVVKRVQDLEQKMKVVE 166
QY 61 NLQDDDFNFKTLKSGQDMQDLNGNNSVTRQKQOQMLEOHLQDVVKRVQDLEQKMKVVE 120
DB 167 NLQDDDFNFKTLKSGQDMQDLNGNNSVTRQKQOQMLEOHLQDVVKRVQDLEQKMKVVE 226
QY 121 AMEYVQKTLTDEBLADWKRPEIACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180
DB 227 AMEYVQKTLTDEBLADWKRPEIACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 286
QY 181 LOOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFT 240
DB 287 LOOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 8
US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 56
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56

Query Match 99.2%; Score 1377; DB 14; Length 770;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCLWEESRLLOTAATAAQAQGGQANHPHTAAVTEKQOQMLEOHLQDVVKRVQDLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQAQGGQANHPHTAAVTEKQOQMLEOHLQDVVKRVQDLEQKMKVVE 166
QY 61 NLQDDDFNFKTLKSGQDMQDLNGNNSVTRQKQOQMLEOHLQDVVKRVQDLEQKMKVVE 120
DB 167 NLQDDDFNFKTLKSGQDMQDLNGNNSVTRQKQOQMLEOHLQDVVKRVQDLEQKMKVVE 226
QY 121 AMEYVQKTLTDEBLADWKRPEIACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180
DB 227 AMEYVQKTLTDEBLADWKRPEIACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 286
QY 181 LOOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFT 240

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Db      287 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
Qy      241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db      347 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 377

RESULT 9
US-10-117-087-2
; Sequence 2, Application US/10117087
; Publication No. US20030166854A1
; GENERAL INFORMATION:
; APPLICANT: SERLUPI-CRESCENZI, Ottaviano
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REFERENCE: SERLUPI-2
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2

Query Match      99.2%; Score 1377; DB 14; Length 770;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 60
Db      107 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 166
Qy      61 NLQDDDFNYKTLKSGQDMQDLNGNOSVTRQKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 120
Db      167 NLQDDDFNYKTLKSGQDMQDLNGNOSVTRQKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 226
Qy      121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESQLOTRQOIKKLEE 180
Db      227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESQLOTRQOIKKLEE 286
Qy      181 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db      287 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
Qy      241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db      347 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 377

RESULT 10
US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match      99.2%; Score 1377; DB 10; Length 793;
Best Local Similarity 99.3%; Pred. No. 9.4e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 60
Db      130 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 189
Qy      61 NLQDDDFNYKTLKSGQDMQDLNGNOSVTRQKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 120
Db      190 NLQDDDFNYKTLKSGQDMQDLNGNOSVTRQKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 249
Qy      121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESQLOTRQOIKKLEE 180
Db      250 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESQLOTRQOIKKLEE 309
Qy      181 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db      310 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 369
Qy      241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db      370 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 400
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; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match      99.2%; Score 1377; DB 9; Length 793;
Best Local Similarity 99.3%; Pred. No. 9.4e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 60
Db      130 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 189
Qy      61 NLQDDDFNYKTLKSGQDMQDLNGNOSVTRQKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 120
Db      190 NLQDDDFNYKTLKSGQDMQDLNGNOSVTRQKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 249
Qy      121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESQLOTRQOIKKLEE 180
Db      250 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESQLOTRQOIKKLEE 309
Qy      181 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db      310 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 369
Qy      241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db      370 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 400

RESULT 11
US-09-925-302-780
; Sequence 780, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match      99.2%; Score 1377; DB 10; Length 793;
Best Local Similarity 99.3%; Pred. No. 9.4e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 60
Db      130 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 189
Qy      61 NLQDDDFNYKTLKSGQDMQDLNGNOSVTRQKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 120
Db      190 NLQDDDFNYKTLKSGQDMQDLNGNOSVTRQKQKQMLEQHLQDVRRKRVQDLEQKMKVVE 249
Qy      121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESQLOTRQOIKKLEE 180
Db      250 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESQLOTRQOIKKLEE 309
Qy      181 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db      310 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 369
Qy      241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db      370 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 400
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RESULT 12
US-10-116-275-329
; Sequence 329, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 329
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Rat
US-10-116-275-329

Query Match 99.0%; Score 1374; DB 15; Length 770;
Best Local Similarity 98.9%; Pred. No. 1.6e-108;
Matches 268; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 60
Db 107 RCLWEESRLLOTAATAAQQGGQANHPHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 166

Qy 61 NLQDDDFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 120
Db 167 NLQDDDFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 286

Qy 181 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 240
Db 287 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 13
US-10-116-275-349
; Sequence 349, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 349
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-116-275-349
Query Match 98.8%; Score 1372; DB 15; Length 770;
Best Local Similarity 98.9%; Pred. No. 2.4e-108;
Matches 268; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 60
Db 107 RCLWEESRLLOTAATAAQQGGQANHPHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 166

Qy 61 NLQDDDFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 120
Db 167 NLQDDDFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 286

Qy 181 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 240
Db 287 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 14
US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US2002019767A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 92.9%; Score 1290; DB 13; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.7e-102;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 60
Db 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 60

Qy 61 NLQDDDFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 120
Db 61 NLQDDDFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 120

Qy 121 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180
Db 121 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180

Qy 181 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 240
Db 181 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 240

Qy 241 TKVRLLVKFPPEL 252

Db 241 TKVRLLVKPEL 252

RESULT 15

US-10-090-185-15
 ; Sequence 15, Application US/10090185
 ; Publication No. US20020197647A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Xiaokui
 ; APPLICANT: Wzieszczyńska, Melissa H
 ; APPLICANT: Horvath, Curt M
 ; APPLICANT: Darnell Jr., James E
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
 ; TITLE OF INVENTION: INTERACTIONS
 ; FILE REFERENCE: 600-1-253
 ; CURRENT APPLICATION NUMBER: US/10/090,185
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: 09/387,418
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-090-185-15

Query Match 87.3%; Score 1212; DB 13; Length 236;
 Best Local Similarity 100.0%; Pred. No. 2.4e-95;
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RCLWEESRLLOTAATAAQGGQANHTAAVVTETKQMLEQHLQDVVKRVQDLEQMKVVE 60
 Db 1 RCLWEESRLLOTAATAAQGGQANHTAAVVTETKQMLEQHLQDVVKRVQDLEQMKVVE 60
 Qy 61 NLQDDDFNYKTLKSQGMQDLNGNOSVTRQKMOLEQMLTALDQMRSSIVSELAGLLS 120
 Db 61 NLQDDDFNYKTLKSQGMQDLNGNOSVTRQKMOLEQMLTALDQMRSSIVSELAGLLS 120
 Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180
 Db 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQOIKKLEE 180
 Qy 181 LQKVSYKGDPIVQHRPMLERIIVELFRLNLMKSAFVVERQCPMPHDPRLVIKTG 236
 Db 181 LQKVSYKGDPIVQHRPMLERIIVELFRLNLMKSAFVVERQCPMPHDPRLVIKTG 236

Search completed: May 5, 2005, 15:17:41
 Job time : 115.139 secs

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; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-369-796-12

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```

Query Match 100.0%; Score 1388; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQGGQANHTAAVTEKQMLEQHLQDVRRKRVQDLEQKMKVVE 60
Db 107 RCLWEESRLLOTAATAAQGGQANHTAAVTEKQMLEQHLQDVRRKRVQDLEQKMKVVE 166

Qy 61 NLQDDFDNYKTLKSGQMDLNGNNSQVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 120
Db 167 NLQDDFDNYKTLKSGQMDLNGNNSQVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEE 286

Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

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RESULT 3
US-08-852-091-12
; Sequence 12, Application US/08852091
; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen

```

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; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-852-091-12

```

```

Query Match 100.0%; Score 1388; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQGGQANHTAAVTEKQMLEQHLQDVRRKRVQDLEQKMKVVE 60
Db 107 RCLWEESRLLOTAATAAQGGQANHTAAVTEKQMLEQHLQDVRRKRVQDLEQKMKVVE 166

Qy 61 NLQDDFDNYKTLKSGQMDLNGNNSQVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 120
Db 167 NLQDDFDNYKTLKSGQMDLNGNNSQVTRQKMQLEQMLTALDQMRSSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEE 286

Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

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RESULT 4
US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan

```


APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-820-754-12

Query Match 100.0%; Score 1388; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEERLLQTAATAAQGGQANHTAAVTEKQMLEQHLQDVVRKVQDLEQKMKVVE 60
Db 107 RCLWEERLLQTAATAAQGGQANHTAAVTEKQMLEQHLQDVVRKVQDLEQKMKVVE 166
Qy 61 NLQDDDFNFKYTKLSQGMQDLNNGNSVTRQKMQLEOMLTALDQMRRSIVSELGLLS 120
Db 167 NLQDDDFNFKYTKLSQGMQDLNNGNSVTRQKMQLEOMLTALDQMRRSIVSELGLLS 226
Qy 121 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTTSIAESQLOTRQIQKLE 180
Db 227 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTTSIAESQLOTRQIQKLE 286
Qy 181 LQQKSVYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLIVITGVQFT 240
Db 287 LQQKSVYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLIVITGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
|||||

Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377
RESULT 5
US-08-956-652-12
Sequence 12, Application US/08956652
Patent No. 6013475
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-956-652-12

Query Match 100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEERLLQTAATAAQGGQANHTAAVTEKQMLEQHLQDVVRKVQDLEQKMKVVE 60
Db 107 RCLWEERLLQTAATAAQGGQANHTAAVTEKQMLEQHLQDVVRKVQDLEQKMKVVE 166
Qy 61 NLQDDDFNFKYTKLSQGMQDLNNGNSVTRQKMQLEOMLTALDQMRRSIVSELGLLS 120
Db 167 NLQDDDFNFKYTKLSQGMQDLNNGNSVTRQKMQLEOMLTALDQMRRSIVSELGLLS 226

QY 121 AMEYVQKTLTDEELADWKRPETACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRPETACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 286
QY 181 LQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 377

RESULT 6
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match 100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RCLWESRLLOTAATAAQQGGOANHTAAVTEKQOMLEQHLQDVKRKRQVDLEQKMKVYE 60
Db 107 RCLWESRLLOTAATAAQQGGOANHTAAVTEKQOMLEQHLQDVKRKRQVDLEQKMKVYE 166
QY 61 NLQDDDFDNFKYKTLKSGQDMQDLNGNNSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLS 120
Db 167 NLQDDDFDNFKYKTLKSGQDMQDLNGNNSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLS 226
QY 121 AMEYVQKTLTDEELADWKRPETACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRPETACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 286
QY 181 LQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 377

RESULT 7
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684

TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-547-12

Query Match 100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVRRKVDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVRRKVDLEQMKVVE 166

Qy 61 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNENWITSIAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNENWITSIAESQLQTRQIKKLEE 286

Qy 181 LQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 8
US-09-364-970-3
; Sequence 3, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-3

Query Match 100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVRRKVDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVRRKVDLEQMKVVE 166

Qy 61 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNENWITSIAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNENWITSIAESQLQTRQIKKLEE 286

Qy 181 LQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 9
US-09-364-970-5
; Sequence 5, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5

Query Match 100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVRRKVDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVRRKVDLEQMKVVE 166

Qy 61 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNENWITSIAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNENWITSIAESQLQTRQIKKLEE 286

Qy 181 LQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 10
US-08-956-653A-12
; Sequence 12, Application US/0895653A
; Patent No. 6338949
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/956,653A
FILING DATE: 11-MAR-1994
CLASSIFICATION: US 08/212,185
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-956-653A-12

Query Match 100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLIQTAAATAAQGGQANHPPTAAVVTKEQQLQHLQDVRRKRVQDLQKMKVVE 60
Db 107 RCLWEESRLIQTAAATAAQGGQANHPPTAAVVTKEQQLQHLQDVRRKRVQDLQKMKVVE 166
Qy 61 NLQDDDFNFYKTLKSGQDMQDLNNGNOSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDDFNFYKTLKSGQDMQDLNNGNOSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRPEIACIGPPNIICLDRLENWITSIAESQLOTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRPEIACIGPPNIICLDRLENWITSIAESQLOTRQOIKKLEE 286
Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVOFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVOFT 346
Qy 241 TKVRLLVKFPPELVQKIKVICIDKSDGVAA 271
Db 347 TKVRLLVKFPPELVQKIKVICIDKSDGVAA 377

RESULT 11
US-08-212-185-12
Sequence 12, Application US/08212185
Patent No. 6605442
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-212-185-12

Query Match 100.0%; Score 1388; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLIQTAAATAAQGGQANHPPTAAVVTKEQQLQHLQDVRRKRVQDLQKMKVVE 60
Db 107 RCLWEESRLIQTAAATAAQGGQANHPPTAAVVTKEQQLQHLQDVRRKRVQDLQKMKVVE 166
Qy 61 NLQDDDFNFYKTLKSGQDMQDLNNGNOSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDDFNFYKTLKSGQDMQDLNNGNOSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRPEIACIGPPNIICLDRLENWITSIAESQLOTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRPEIACIGPPNIICLDRLENWITSIAESQLOTRQOIKKLEE 286
Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVOFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVOFT 346
Qy 241 TKVRLLVKFPPELVQKIKVICIDKSDGVAA 271
Db 347 TKVRLLVKFPPELVQKIKVICIDKSDGVAA 377

RESULT 12
PCT-US95-17025-12

; Sequence 12, Application PC/TUS9517025
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17025
; FILING DATE: 28-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-17025-12

Query Match 100.0%; Score 1388; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLQTAATAAQGGQANHPTAAVVTKEQQLQHLQDVVRKRVQDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHPTAAVVTKEQQLQHLQDVVRKRVQDLEQMKVVE 166
Qy 61 NLQDDFFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDFFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 226
Qy 121 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNNWITSLSAQLOTRQIQKLEE 180
Db 227 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNNWITSLSAQLOTRQIQKLEE 286
Qy 181 LQKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHMDRPLVKTGVQFT 240
Db 287 LQKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHMDRPLVKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 377

RESULT 13
US-08-416-581B-9
; Sequence 9, Application US/08416581B

; Patent No. 5719042
; GENERAL INFORMATION:
; APPLICANT: Kishimoto, Tadimitsu
; APPLICANT: Akira, Shizuo
; TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,581B
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-65825/1994
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-37891
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-416-581B-9

Query Match 99.2%; Score 1377; DB 1; Length 770;
Best Local Similarity 99.3%; Pred. No. 1.7e-117;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RCLWEESRLQTAATAAQGGQANHPTAAVVTKEQQLQHLQDVVRKRVQDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHPTAAVVTKEQQLQHLQDVVRKRVQDLEQMKVVE 166
Qy 61 NLQDDFFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDFFNYKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 226
Qy 121 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNNWITSLSAQLOTRQIQKLEE 180
Db 227 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNNWITSLSAQLOTRQIQKLEE 286
Qy 181 LQKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHMDRPLVKTGVQFT 240
Db 287 LQKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHMDRPLVKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 377

RESULT 14
US-09-012-710-8
; Sequence 8, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moareffi, Ismail
; APPLICANT: Darnell, Jr., James E.

APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
CORRESPONDENCE ADDRESS: 13
NUMBER OF SEQUENCES: 13
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-012-710-8

Query Match 99.2%; Score 1377; DB 3; Length 770;
Best Local Similarity 99.3%; Pred. No. 1.7e-117; Indels 0; Gaps 0;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RCLWEESRLLOTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVVRKRVQDLEQMKVVE 60
Db 107 RCLWEESRLLOTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVVRKRVQDLEQMKVVE 166
Qy 61 NLODDDFNYKTLKSGQDMQDLNNGNQSVTQKMQOLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLODDDFNYKTLKSGQDMQDLNNGNQSVTQKMQOLEQMLTALDQRRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQIKKLEE 286
Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRLVKTGVQFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRLVKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVICDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICDKSDGVAA 377

RESULT 15

US-09-556-273-8
Sequence 8, Application US/09556273
Patent No. 6312887
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A

TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-556-273-8

Query Match 99.2%; Score 1377; DB 3; Length 770;
Best Local Similarity 99.3%; Pred. No. 1.7e-117; Indels 0; Gaps 0;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RCLWEESRLLOTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVVRKRVQDLEQMKVVE 60
Db 107 RCLWEESRLLOTAATAAQGGQANHPAAVVTKEQOMLEQHLQDVVRKRVQDLEQMKVVE 166
Qy 61 NLODDDFNYKTLKSGQDMQDLNNGNQSVTQKMQOLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLODDDFNYKTLKSGQDMQDLNNGNQSVTQKMQOLEQMLTALDQRRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQIKKLEE 286
Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRLVKTGVQFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRLVKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVICDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICDKSDGVAA 377

Search completed: May 5, 2005, 14:58:52
Job time : 41.8094 secs

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	1388	100.0	271	4	AAy72841	Mouse Sta
2	1388	100.0	770	2	AAr72082	Mouse Sta
3	1388	100.0	770	2	AAw03176	Mouse Sta
4	1377	99.2	720	5	AAE22055	Human Sta
5	1377	99.2	769	5	ABb57164	Mouse isc
6	1377	99.2	769	5	AAE22054	Human Sta
7	1377	99.2	769	5	AAE22056	Human pro
8	1377	99.2	770	2	AAr82295	Mouse liv
9	1377	99.2	770	2	AAb12377	Human STA
10	1377	99.2	770	3	AAE132377	N-termina
11	1377	99.2	770	5	AAE14652	Murine ST
12	1377	99.2	770	5	ABg69497	Human bai
13	1377	99.2	770	6	ABU10476	Mouse STA
14	1377	99.2	770	8	ADN04365	Human PRO
15	1377	99.2	770	8	ADp54789	Antipsoi
16	1377	99.2	793	3	AAE58442	Lung canc
17	1374	99.0	770	7	ADd44738	Rat Prote
18	1372	98.8	770	2	AAE82293	Human pla
19	1372	98.8	770	4	AAE11964	Human sig
20	1372	98.8	770	5	AAE15174	Human Sta
21	1372	98.8	770	7	ADd44740	Human Pro
22	1290	92.9	252	4	AAy72846	Mouse Sta
23	1212	87.3	236	4	AAy72847	Mouse Sta
24	1172	84.4	229	4	AAy72850	Mouse Sta
25	1168	84.1	229	4	AAy72863	Mouse Sta

CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 271 AA;

Query Match 100.0%; Score 1388; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2.7e-116;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCLWEESRLIQTATAAQAQGGQANHPHTAAVVTKEQMLEQHLQDVRRKRVQDLEQMKVVE 60
 DB 1 RCLWEESRLIQTATAAQAQGGQANHPHTAAVVTKEQMLEQHLQDVRRKRVQDLEQMKVVE 60
 QY 61 NLQDDDFNFKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
 DB 61 NLQDDDFNFKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
 QY 121 AMEVOKTLTDEELADWKRRPEIACIGGPNICLDRLNWTSLAESQLTROQIKKLEE 180
 DB 121 AMEVOKTLTDEELADWKRRPEIACIGGPNICLDRLNWTSLAESQLTROQIKKLEE 180
 QY 181 LQKVSYKGDPIVOHREPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 240
 DB 181 LQKVSYKGDPIVOHREPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 240
 QY 241 TKVRLLVKPELNYQLKIKVICIDKSDGVAA 271
 DB 241 TKVRLLVKPELNYQLKIKVICIDKSDGVAA 271

RESULT 2
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX
 AC AAR72082;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX
 XX Mouse Stat3 (19sf6).
 XX
 KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX
 OS Mus sp.
 XX
 XX WO9508629-A1.
 XX
 PD 30-MAR-1995.
 XX
 XX 26-SEP-1994; 94WO-US010849.
 XX
 XX 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126595.
 PR 11-MAR-1994; 94US-00212184.
 PR 11-MAR-1994; 94US-00212185.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 XX WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 XX
 XX Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX

PS Claim 1; Page 107-110; 160pp; English.
 XX
 CC A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 1388; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1.1e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCLWEESRLIQTATAAQAQGGQANHPHTAAVVTKEQMLEQHLQDVRRKRVQDLEQMKVVE 60
 DB 107 RCLWEESRLIQTATAAQAQGGQANHPHTAAVVTKEQMLEQHLQDVRRKRVQDLEQMKVVE 166
 QY 61 NLQDDDFNFKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
 DB 167 NLQDDDFNFKTLKSQGMQDLNNGNSVTRQKMQLEQMLTALDQRRSIVSELAGLLS 226
 QY 121 AMEVOKTLTDEELADWKRRPEIACIGGPNICLDRLNWTSLAESQLTROQIKKLEE 180
 DB 227 AMEVOKTLTDEELADWKRRPEIACIGGPNICLDRLNWTSLAESQLTROQIKKLEE 286
 QY 181 LQKVSYKGDPIVOHREPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 240
 DB 287 LQKVSYKGDPIVOHREPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT 346
 QY 241 TKVRLLVKPELNYQLKIKVICIDKSDGVAA 271
 DB 347 TKVRLLVKPELNYQLKIKVICIDKSDGVAA 377

RESULT 3
 AAW03176
 ID AAW03176 standard; protein; 770 AA.
 XX
 AC AAW03176;
 XX
 DT 24-OCT-1996 (first entry)
 DT
 DE Mouse STAT4.
 XX
 KW STAT; STAT4; signal transducer and activator of transcription;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW autoimmune disease; antagonist; therapy.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH Domain 398..508
 FT /label= DNA binding domain
 FT /note= "Claim 3, page 110"
 XX
 PN WO9620954-A2.
 XX
 XX 11-JUL-1996.
 XX
 XX 28-DEC-1995; 95WO-US017025.
 XX
 XX 06-JAN-1995; 95US-00369796.
 PR
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Darnell JE, Wen Z, Horvath CM, Zhong Z;
 XX WPI; 1996-333941/33.
 DR

QY 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVLTGTVQFT 240
DB 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVLTGTVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVICIDKSDGVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVICIDKSDGVAA 377

RESULT 5
ABB57164
ID ABB57164 standard; protein; 769 AA.
XX
AC ABB57164;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related protein sequence SEQ ID NO:398.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP004192.
XX
PR 18-MAY-2000; 2000JP-00145977.
XX
PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Iehikawa K, Asai S, Takahashi Y, Nagata T, Iehii Y;
XX
DR WPI; 2002-034733/04.
DR N-PSDB; ABI99454.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
PS Claim 2; Page 1084-1087; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI999202 to ABI99912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
SQ Sequence 769 AA;

Query Match 99.2%; Score 1377; DB 5; Length 769;
Best Local Similarity 99.3%; Pred. No. 1e-114;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCLWEERLLQTAATAAQGGQANHPAAVTEKQQLQVRRKRVQDLEQKMKVVE 60
DB 107 RCLWEERLLQTAATAAQGGQANHPAAVTEKQQLQVRRKRVQDLEQKMKVVE 166
QY 61 NLQDDFFNYKTLKSGDMQDLNNGNSVTRQKMQOLEMLTALDQMRISIVSELGALLS 120

DB 167 NLQDDFFNYKTLKSGDMQDLNNGNSVTRQKMQOLEMLTALDQMRISIVSELGALLS 226
QY 121 AMEYVOKTITDEBLADWKRPETACIGGPPNICLDLENWITSLAESQLQTRQIKKLEE 180
DB 227 AMEYVOKTITDEBLADWKRRQACIGGPPNICLDLENWITSLAESQLQTRQIKKLEE 286
QY 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVLTGTVQFT 240
DB 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVLTGTVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVICIDKSDGVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVICIDKSDGVAA 377

RESULT 6
AAE22054
ID AAE22054 standard; protein; 769 AA.
XX
AC AAE22054;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human Stat3 protein.
XX
KW Human; signal transducer and activator of transcription 3; ischaemia;
KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
KW shock; chronic active hepatitis; adult respiratory distress syndrome;
KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
KW polyomyelitis; rheumatoid arthritis; autoimmune infertility; anaemia;
KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
KW cirrhosis; hypoproliferative disorder; lesion.
XX
OS Homo sapiens.
XX
PN WO200220032-A1.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028254.
XX
PR 08-SEP-2000; 2000US-0231212P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UYSF-) UNIV SOUTH FLORIDA.
XX
PI Yu H, Pardoll D, Jove R, Dalton W;
XX
DR WPI; 2002-362218/39.
DR N-PSDB; AAD35065.
XX
PT Modulating angiogenesis and an immune response in an individual, for
PT treating a hypoxic or ischemic condition, comprises administering a
PT compound that modulates the activity of a signal transducer and activator
PT of transcription 3.
XX
PS Disclosure; Page 83-85; 94pp; English.
XX
CC The invention relates to a method of modulating angiogenesis and immune
CC response. Method involves administering to an individual a compound that
CC modulate the activity of signal transducer and activator of transcription
CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
CC hypoxic or ischaemic condition or disorder which is the result of stroke,
CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,

CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein
 XX
 SQ Sequence 769 AA;

Query Match 99.2%; Score 1377; DB 5; Length 769;
 Best Local Similarity 99.3%; Pred. No. 1e-114;
 Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCLWEESRLQTAATAAQGGQANHPPTAAVTEKQOMLEQHLQDVRKRVQDLQKMKVE 60
 DB 107 RCLWEESRLQTAATAAQGGQANHPPTAAVTEKQOMLEQHLQDVRKRVQDLQKMKVE 166
 QY 61 NLQDDDFNFKTLKSGQDMQDLNGNOSVTRQKQOMLEQHLQDVRKRVQDLQKMKVE 120
 DB 167 NLQDDDFNFKTLKSGQDMQDLNGNOSVTRQKQOMLEQHLQDVRKRVQDLQKMKVE 226
 QY 121 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNENWITSLSAQLOTRQIKLEE 180
 DB 227 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNENWITSLSAQLOTRQIKLEE 286
 QY 181 LQOKVSYKGDPIVQHRPMLBERIVELFRNLKMSAFVVERQPCMPHDPRLVITGVQFT 240
 DB 287 LQOKVSYKGDPIVQHRPMLBERIVELFRNLKMSAFVVERQPCMPHDPRLVITGVQFT 346
 QY 241 TKVRLVKFPFLNYQLKIKVCIDKSGDVAA 271
 DB 347 TKVRLVKFPFLNYQLKIKVCIDKSGDVAA 377

RESULT 7
 AAE22056
 ID AAE22056 standard; protein; 769 AA.

XX AAE22056;
 XX
 XX 25-JUL-2002 (first entry)
 XX Human protein related to angiogenesis regulation.
 DE Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 OS Homo sapiens.
 XX WO200220032-A1.
 XX

PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028254.
 XX
 PR 08-SEP-2000; 2000US-0231212P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSP-) UNIV SOUTH FLORIDA.
 XX
 PI Yu H, Pardoll D, Jove R, Dalton W;
 XX WPI; 2002-362218/39.
 DR
 XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX
 PS Disclosure; Page 83-85; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation
 XX
 SQ Sequence 769 AA;

Query Match 99.2%; Score 1377; DB 5; Length 769;
 Best Local Similarity 99.3%; Pred. No. 1e-114;
 Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCLWEESRLQTAATAAQGGQANHPPTAAVTEKQOMLEQHLQDVRKRVQDLQKMKVE 60
 DB 107 RCLWEESRLQTAATAAQGGQANHPPTAAVTEKQOMLEQHLQDVRKRVQDLQKMKVE 166
 QY 61 NLQDDDFNFKTLKSGQDMQDLNGNOSVTRQKQOMLEQHLQDVRKRVQDLQKMKVE 120
 DB 167 NLQDDDFNFKTLKSGQDMQDLNGNOSVTRQKQOMLEQHLQDVRKRVQDLQKMKVE 226
 QY 121 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNENWITSLSAQLOTRQIKLEE 180
 DB 227 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNENWITSLSAQLOTRQIKLEE 286
 QY 181 LQOKVSYKGDPIVQHRPMLBERIVELFRNLKMSAFVVERQPCMPHDPRLVITGVQFT 240
 DB 287 LQOKVSYKGDPIVQHRPMLBERIVELFRNLKMSAFVVERQPCMPHDPRLVITGVQFT 346
 QY 241 TKVRLVKFPFLNYQLKIKVCIDKSGDVAA 271
 XX

Db 347 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 377
|||||
RESULT 10
AAB12377
ID AAB12377 standard; peptide; 770 AA.
XX AAB12377;
XX
XX 08-NOV-2000 (first entry)
XX N-terminal domain of murine STAT-3 protein.
XX
XX STAT; signal transducer and activator of transcription; crystal;
XX drug design; murine.
XX
XX Mus sp.
XX
FH Key Location/Qualifiers
Region 4..9
FT /label= Alpha helix 1
FT 12..21
FT /label= Alpha helix 2
FT 19..21
FT /label= 3(10) helix of alpha helix 2
FT 28..33
FT /label= Alpha helix 3
FT 35..40
FT /label= Alpha helix 4
FT 43..47
FT /label= Alpha helix 5
FT 50..73
FT /label= Alpha helix 6
FT 77..96
FT /label= Alpha helix 7
FT 99..119
FT /label= Alpha helix 8
XX
XX US6087478-A.
XX
XX 11-JUL-2000.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX WPI; 2000-505108/45.
XX
XX New crystals of an N-terminal fragment of a signal transducer and
XX activator of transcription that effectively diffracts x-rays, useful for
XX drug screening and development.
XX
XX Disclosure; Fig 1; 42pp; English.
XX
XX The present invention relates to a crystal of an N-terminal fragment of a
XX signal transducer and activator of transcription (STAT) protein. The
XX crystal effectively diffracts x-rays, allowing the determination of the
XX atomic coordinates of the N-terminal domain to a resolution of greater
XX than 5.0 Angstroms. The present sequence is the N-terminal domain of the
XX murine STAT 3 protein. The N-terminal domain enables STAT dimers to
XX interact and bind DNA cooperatively, a mechanism important for gene
XX activation. The crystals are useful in drug screening and development by
XX selecting a potential drug by performing rational drug design with the 3-
XX dimensional structure determined for the crystal
XX
XX Sequence 770 AA;
XX
XX Query Match 99.2%; Score 1377; DB 3; Length 770;

Best Local Similarity 99.3%; Pred. No. 1e-114;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCLWEESRLLOTATAAQAQGGQANHPHTAAVVTETKQQLMEOHLOQVVRKRVQDLEQMKVVE 60
DB 107 RCLWEESRLLOTATAAQAQGGQANHPHTAAVVTETKQQLMEOHLOQVVRKRVQDLEQMKVVE 166
QY 61 NLQDDDFNYKTLKSGQDMQDLNNGNSVTRQKMQQLEQMLTALDQRRSTVSELGLLS 120
DB 167 NLQDDDFNYKTLKSGQDMQDLNNGNSVTRQKMQQLEQMLTALDQRRSTVSELGLLS 226
QY 121 AMEYVQKTLTDEELADWKRPEIACIGGPNICLDRLNWTSLAESQLOTRQIKKLEE 180
DB 227 AMEYVQKTLTDEELADWKRPEIACIGGPNICLDRLNWTSLAESQLOTRQIKKLEE 286
QY 181 LQKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLVITGVQFT 240
DB 287 LQKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLVITGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 377
RESULT 11
AAB14652
ID AAB14652 standard; protein; 770 AA.
XX AAE14652;
XX
XX 16-JUL-2002 (first entry)
XX Murine STAT3 protein.
XX
XX Signal transducer and activator of transcription; STAT3;
XX drug development; drug discovery; crystal; inflammation; allergy; asthma;
XX leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity;
XX viral disease; growth retardation; murine.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
Domain 1..130
FT /note= "Conserved N-terminal domain of the STAT family"
XX
XX US6312887-B1.
XX
XX 06-NOV-2001.
XX
XX 24-APR-2000; 2000US-00556273.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX WPI; 2002-033337/04.
XX
XX Identifying compounds that bind to signal transducer and activator of
XX transcription proteins, useful for the production of new drugs.
XX
XX Example; Col 47-50; 44pp; English.
XX
XX The invention relates to methods for detecting compounds that bind to
XX signal transducer and activator of transcription (STAT) proteins for the
XX discovery and development of new drug compounds based on the structural
XX properties of the protein crystal. The methods include: identifying a
XX compound that binds to the N-terminal domain of a STAT protein,
XX identifying a compound that enhances or diminishes the binding of the
XX dimeric STAT proteins to each other and/or their nucleic acid binding
XX site; or identifying a compound that enhances or diminishes the ability
XX of STAT protein dimers to induce the expression of a gene operably under

CC the control of a promoter containing at least two adjacent weak binding
 CC sites for STAT protein dimers. The methods are used for identifying new
 CC drugs. An antagonist of STAT N-terminal dimeric interactions that
 CC inhibits the binding of the STAT dimers to adjacent weak binding sites on
 CC a promoter of a gene, could be useful as drugs in the treatment of
 CC diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other
 CC hand, an agonist of N-terminal dimeric interactions between STAT dimers,
 CC can be used as drugs in the treatment of diseases e.g. anaemia,
 CC neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and
 CC growth retardation. The present sequence is murine STAT3 protein
 XX
 XX Sequence 770 AA;

Query Match 99.2%; Score 1377; DB 5; Length 770;
 Best Local Similarity 99.3%; Pred. No. 1e-114;
 Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQQLMQLDQVRRKRVQDLQKMKVVE 60
 Db 107 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQQLMQLDQVRRKRVQDLQKMKVVE 166
 Qy 61 NLQDDDFNFYKTLKSGQMDLNGNNSVTRQKQQLMQLDQVRRKRVQDLQKMKVVE 120
 Db 167 NLQDDDFNFYKTLKSGQMDLNGNNSVTRQKQQLMQLDQVRRKRVQDLQKMKVVE 226
 Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSIAESQLQTRQIKKLEE 180
 Db 227 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSIAESQLQTRQIKKLEE 286
 Qy 181 LQOKVSKGDPVQHRPMLERIVELFRNLKMSAFVVERPCMPMPHDPRLVKTGVQFT 240
 Db 287 LQOKVSKGDPVQHRPMLERIVELFRNLKMSAFVVERPCMPMPHDPRLVKTGVQFT 346
 Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
 Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 12
 ABG69497
 ID ABG69497 standard; protein; 770 AA.
 XX
 AC ABG69497;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human bait protein STAT3.
 XX
 KW Human; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
 KW non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
 KW protein-protein interaction map; PIM; anorectic; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 FN WO200253726-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 28-DEC-2001; 2001WO-EP015423.
 XX
 PR 02-JAN-2001; 2001US-0259377P.
 XX
 PA (HYBR-) HYBRIGENICS.
 PA (CNRS) CENT NAT RECH SCI.
 XX
 XX Legrain P, Marullo S, Jockers R;
 XX
 DR WPI; 2002-583612/62.
 DR N-PSDB; ABS51033.
 XX
 PT Novel complex of protein-protein interactions in adipocyte cells for
 PT identifying compounds that modulate the protein-protein interactions and
 PT useful for treating obesity and metabolic disorders.

XX
 PS
 XX
 CC Claim 1; Page 54; 125pp; English.
 CC The invention relates to a complex of protein-protein interactions
 CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
 CC defined in the specification, or polynucleotides in adipocytes encoding the
 CC for the polypeptides. Also included are a recombinant cell expressing the
 CC interacting polypeptides and a method of selecting a modulating compound
 CC in adipocyte cells, by cultivating a recombinant host cell on a selective
 CC medium containing a modulating compound and a reporter gene the
 CC expression of which is toxic for the recombinant host cell which is
 CC transformed with two vectors, where the first vector comprises a
 CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain
 CC and the second vector comprising a polynucleotide encoding a second
 CC hybrid polypeptide and an activating domain that activates the toxic
 CC reporter gene, when the first and second hybrid polypeptides interact and
 CC selecting the modulating compound which inhibits the growth of the
 CC recombinant host cell (i.e. using the yeast two-hybrid system). The
 CC complexes are useful for identifying compounds that modulate the protein-
 CC protein interactions and useful for treating obesity and metabolic
 CC disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
 CC compound isolated by the method is useful for treating and preventing
 CC obesity or metabolic diseases. The interactions between the proteins of
 CC the complex further define a set of selected interacting domains, SID.
 CC The present sequence represents a member of the protein complex of the
 CC invention, used as the bait protein in the yeast two-hybrid assay
 XX
 XX Sequence 770 AA;

Query Match 99.2%; Score 1377; DB 5; Length 770;
 Best Local Similarity 99.3%; Pred. No. 1e-114;
 Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQQLMQLDQVRRKRVQDLQKMKVVE 60
 Db 107 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQQLMQLDQVRRKRVQDLQKMKVVE 166
 Qy 61 NLQDDDFNFYKTLKSGQMDLNGNNSVTRQKQQLMQLDQVRRKRVQDLQKMKVVE 120
 Db 167 NLQDDDFNFYKTLKSGQMDLNGNNSVTRQKQQLMQLDQVRRKRVQDLQKMKVVE 226
 Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSIAESQLQTRQIKKLEE 180
 Db 227 AMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSIAESQLQTRQIKKLEE 286
 Qy 181 LQOKVSKGDPVQHRPMLERIVELFRNLKMSAFVVERPCMPMPHDPRLVKTGVQFT 240
 Db 287 LQOKVSKGDPVQHRPMLERIVELFRNLKMSAFVVERPCMPMPHDPRLVKTGVQFT 346
 Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
 Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 13
 ABU10476
 ID ABU10476 standard; protein; 770 AA.
 XX
 AC ABU10476;
 XX
 DT 06-AUG-2003 (first entry)
 XX
 DE Mouse STAT3 protein.
 XX
 KW Mouse; signal transducer and activator of transcription; drug design;
 KW drug screening; STAT-STAT dimer interaction; STAT3.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 4..9
 FT /label= alpha_helix_1
 FT Region 12..21

```
FT FT /label= alpha_helix_2
FT FT /note= "Residues 19-21 form a 3 helix"
FT FT 28..33
FT FT /label= alpha_helix_3
FT FT 35..40
FT FT /label= alpha_helix_4
FT FT 43..47
FT FT /label= alpha_helix_5
FT FT 50..73
FT FT /label= alpha_helix_6
FT FT /note= "Residues 57, 61, 64, 68 and 71 contribute to
FT FT packing of the coiled-coil"
FT FT 77..96
FT FT /label= alpha_helix_7
FT FT /note= "Residues 79, 83, 86, 90 and 94 contribute to
FT FT packing of the coiled-coil"
FT FT 99..119
FT FT /label= alpha_helix_8
FT FT
XX XX US2003003563-A1.
XX XX
XX XX 02-JAN-2003.
XX XX
XX XX 19-OCT-2001; 2001US-00045792.
XX XX
XX XX 23-JAN-1998; 98US-00012710.
XX XX
XX XX 24-APR-2000; 2000US-00556273.
XX XX
XX XX (VINK/) VINKEMEIER U.
XX XX (MOAR/) MOAREFI I.
XX XX (DARN/) DARNELL J E.
XX XX (KURI/) KURIYAN J.
XX XX
XX XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX XX
XX XX WPI; 2003-447354/42.
XX XX
XX XX New crystal having an N-terminal domain of a STAT protein performing X-
XX XX ray crystallographic studies, useful for screening drugs that enhance or
XX XX inhibit STAT-STAT dimer interactions.
XX XX
XX XX Disclosure; Page 25-26; 46pp; English.
XX XX
XX XX The invention relates to a crystal of an N-terminal domain of signal
XX XX transducer and activator of transcription (STAT) protein, where the
XX XX crystal effectively diffracts X-rays for the determination of the atomic
XX XX coordinates of the N-terminal domain of the STAT protein to a resolution
XX XX of greater than 5.0 Angstrom. The methods and compositions are useful for
XX XX the design and screening of drugs that enhance or inhibit STAT-STAT dimer
XX XX interactions. The present sequence represents the amino acid sequence of
XX XX mouse STAT3 protein
XX XX
XX XX Sequence 770 AA;
XX XX
XX XX Query Match 99.2%; Score 1377; DB 6; Length 770;
XX XX Best Local Similarity 99.3%; Pred. No. 1e-114;
XX XX Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX XX 1 RCLWEESRLLTATAAQQGGQANHPAAVTEKQMLEQHLQDVRKRVQDLEQKMKVVE 60
XX XX 107 RCLWEESRLLTATAAQQGGQANHPAAVTEKQMLEQHLQDVRKRVQDLEQKMKVVE 166
XX XX
XX XX 61 NLQDDDFNFKTLKSGQMDLNGNNSVTRQKMQQLEQMLTALDQMRSSIVSELAGLLS 120
XX XX 167 NLQDDDFNFKTLKSGQMDLNGNNSVTRQKMQQLEQMLTALDQMRSSIVSELAGLLS 226
XX XX
XX XX 121 AMEYVQKTLTDEELADWKRREPEIACIGGPPNCLDRLENWITSLAESQLQTRQIKKLEE 180
XX XX 167 NLQDDDFNFKTLKSGQMDLNGNNSVTRQKMQQLEQMLTALDQMRSSIVSELAGLLS 226
XX XX
XX XX 121 AMEYVQKTLTDEELADWKRREPEIACIGGPPNCLDRLENWITSLAESQLQTRQIKKLEE 180
XX XX 227 AMEYVQKTLTDEELADWKRREPEIACIGGPPNCLDRLENWITSLAESQLQTRQIKKLEE 286
XX XX
XX XX 181 LQQKSVKGDPIVOHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVKTGVQFT 240
XX XX 227 AMEYVQKTLTDEELADWKRREPEIACIGGPPNCLDRLENWITSLAESQLQTRQIKKLEE 286
XX XX
XX XX 181 LQQKSVKGDPIVOHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVKTGVQFT 240
XX XX 287 LQQKSVKGDPIVOHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVKTGVQFT 346
XX XX
```

```
Qy 241 TKVRLLYKFPPELNYQLKIKVCIDKDSGDVAA 271
Db 347 TKVRLLYKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 14
ADN04365
ID ADN04365 standard; protein; 770 AA.
XX
XX ADN04365;
XX
XX 01-JUL-2004 (first entry)
XX
XX Antipsoriatic protein sequence #377.
XX
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2004028479-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030907.
XX
XX 25-SEP-2002; 2002US-0414006P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX Wu TD;
XX
XX WPI; 2004-305105/28.
XX
XX N-PSDB; ADN04364.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
XX pharmaceutical composition for diagnosing or treating psoriasis in a
XX mammal.
XX
XX Claim 9; SEQ ID NO 759; 3069pp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
XX treating psoriasis or a sequence having at least 80% identity to the
XX above sequences. The nucleic acid is useful for preparing a composition
XX for diagnosing or treating psoriasis in a mammal. This sequence
XX corresponds to one of the polypeptides of the invention.
XX
XX Sequence 770 AA;
XX
XX Query Match 99.2%; Score 1377; DB 8; Length 770;
XX XX Best Local Similarity 99.3%; Pred. No. 1e-114;
XX XX Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX XX 1 RCLWEESRLLTATAAQQGGQANHPAAVTEKQMLEQHLQDVRKRVQDLEQKMKVVE 60
XX XX 107 RCLWEESRLLTATAAQQGGQANHPAAVTEKQMLEQHLQDVRKRVQDLEQKMKVVE 166
XX XX
XX XX 61 NLQDDDFNFKTLKSGQMDLNGNNSVTRQKMQQLEQMLTALDQMRSSIVSELAGLLS 120
XX XX 167 NLQDDDFNFKTLKSGQMDLNGNNSVTRQKMQQLEQMLTALDQMRSSIVSELAGLLS 226
XX XX
XX XX 121 AMEYVQKTLTDEELADWKRREPEIACIGGPPNCLDRLENWITSLAESQLQTRQIKKLEE 180
XX XX 227 AMEYVQKTLTDEELADWKRREPEIACIGGPPNCLDRLENWITSLAESQLQTRQIKKLEE 286
XX XX
XX XX 181 LQQKSVKGDPIVOHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVKTGVQFT 240
XX XX 287 LQQKSVKGDPIVOHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVKTGVQFT 346
XX XX
XX XX 241 TKVRLLYKFPPELNYQLKIKVCIDKDSGDVAA 271
XX XX 347 TKVRLLYKFPPELNYQLKIKVCIDKDSGDVAA 377
```


RESULT 15
ADP54789
ID ADP54789 standard; protein; 770 AA.
XX
XX AC ADP54789;
XX DT 18-NOV-2004 (first entry)
XX DE Human PRO protein sequence SEQ ID NO:765.
XX KW human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW virucide; gene therapy.
XX OS Homo sapiens.
XX DN WO2004039956-A2.
XX PD 13-MAY-2004.
XX PF 28-OCT-2003; 2003WO-US034381.
XX PR 29-OCT-2002; 2002US-0422472P.
XX PA (GETH) GENENTECH INC.
XX PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX WI: 2004-376182/35.
DR N-PSDB; ADP54788.
XX New PRO polynucleotides and polypeptides, useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.
XX
XX Claim 1; SEQ ID NO 765; 3009pp; English.
XX The present invention describes an isolated PRO nucleic acid (1). Also
CC described: (1) a vector comprising (1); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianaemic, antiarthritic,
CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (1) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO protein from the present invention.

SQL Sequence 770 AA;
Query Match 99.2%; Score 1377; DB 8; Length 770;
Best Local Similarity 99.3%; Pred. No. 1e-114;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCLWEESRLLOTAATAAQQGGQANHPATAAVVTEKQQLLEQHLQDVRRKRVODLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQQGGQANHPATAAVVTEKQQLLEQHLQDVRRKRVODLEQKMKVVE 166
QY 61 NLODDDFNYKTLKSGQDMODLNGNNSQSVTRQKQQLLEQMLTALDQWRRSIVSELAGLLS 120
DB 167 NLODDDFNYKTLKSGQDMODLNGNNSQSVTRQKQQLLEQMLTALDQWRRSIVSELAGLLS 226
QY 121 AMEVVOKTLTDEELADWKRPETACIGGPPNICLDRLNNWITSLSBSQLOTROQIKKLEE 180
DB 227 AMEVVOKTLTDEELADWKRRQQTACIGGPPNICLDRLNNWITSLSBSQLOTROQIKKLEE 286
QY 181 LQOKVSYKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
DB 287 LQOKVSYKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377
Search completed: May 5, 2005, 15:01:10
Job time : 85.1694 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 50.566 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-21

Perfect score: 477
Sequence: 1 VQLEQKKVVENLQDDFF.....YVQKLTDELDWKRPEI 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1980s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	95	4 AAY72853	Aay72853 Mouse Sta
2	477	100.0	128	4 AAY72852	Aay72852 Mouse Sta
3	477	100.0	143	4 AAY72849	Aay72849 Mouse Sta
4	477	100.0	176	4 AAY72848	Aay72848 Mouse Sta
5	477	100.0	213	4 AAY72851	Aay72851 Mouse Sta
6	477	100.0	223	4 AAY72854	Aay72854 Mouse Sta
7	477	100.0	228	4 AAY72861	Aay72861 Mouse Sta
8	477	100.0	229	4 AAY72860	Aay72860 Mouse Sta
9	477	100.0	229	4 AAY72850	Aay72850 Mouse Sta
10	477	100.0	229	4 AAY72863	Aay72863 Mouse Sta
11	477	100.0	229	4 AAY72862	Aay72862 Mouse Sta
12	477	100.0	236	4 AAY72847	Aay72847 Mouse Sta
13	477	100.0	252	4 AAY72846	Aay72846 Mouse Sta
14	477	100.0	271	4 AAY72841	Aay72841 Mouse Sta
15	477	100.0	770	2 AAY72082	Aay72082 Mouse Sta
16	477	100.0	770	2 AAW03176	Aaw03176 Mouse Sta
17	466	97.7	720	5 AAE22055	Aae22055 Human Sta
18	466	97.7	769	5 ABB57164	Abb57164 Mouse isc
19	466	97.7	769	5 AAE22054	Aae22054 Human Sta
20	466	97.7	769	5 AAE22056	Aae22056 Human pro
21	466	97.7	770	2 AAR82995	Aar82995 Mouse liv
22	466	97.7	770	2 AAR82993	Aar82993 Human pla
23	466	97.7	770	2 AAY03768	Aay03768 Human Sta
24	466	97.7	770	3 AAB12377	Aab12377 N-termina
25	466	97.7	770	4 AAB19964	Aab19964 Human sig

26	466	97.7	770	5 AAE14652	Aae14652 Murine ST
27	466	97.7	770	5 ABG69497	Abg69497 Human bai
28	466	97.7	770	5 AAE15174	Aae15174 Human Sta
29	466	97.7	770	6 ABU10476	Abu10476 Mouse STA
30	466	97.7	770	7 ADD44738	Add44738 Rat Prote
31	466	97.7	770	7 ADD44740	Add44740 Human Pro
32	466	97.7	770	8 ADN04365	Adn04365 Antipsoxi
33	466	97.7	770	8 ADP54789	Adp54789 Human PRO
34	466	97.7	793	3 AAB58442	Aab58442 Lung canc
35	278	58.3	185	4 AAY72855	Aay72855 Mouse Sta
36	173	36.3	423	6 ABR47598	Abr47598 Breast ca
37	173	36.3	704	2 AAW01102	Aaw01102 Signal tr
38	173	36.3	748	2 AAW01101	Aaw01101 Signal tr
39	173	36.3	748	4 AAB19965	Aab19965 Human sig
40	173	36.3	748	5 AAE15175	Aae15175 Human Sta
41	173	36.3	748	6 ABR47599	Abr47599 Breast ca
42	173	36.3	748	8 ADL82891	Adl82891 Human PRO
43	173	36.3	748	8 ADP13003	Adp13003 Protein e
44	173	36.3	748	8 ADRI4089	Adri4089 Human NF-
45	173	36.3	748	8 ADRI4361	Adri4361 Human NF-

ALIGNMENTS

RESULT 1

AAV72853

ID AAY72853 standard; protein; 95 AA.

AC AAY72853;

XX 31-MAY-2001 (first entry)

XX Mouse Stat3 protein fragment #11 (155-249 amino acids).

XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
cellular transformation; dysproliferative disease; cancer; psoriasis;
therapy.

OS Mus musculus.

XX WO200116605-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023822.

XX 31-AUG-1999; 99US-00387418.

XX (UYRQ) UNIV ROCKEFELLER.

XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;

XX WPI; 2001-226705/23.

XX Identifying an agent for use in modulating the interaction between
transcription factor c-Jun and a Stat3 protein.

XX Claim 65; Page 78; 86pp; English.

The present sequence is mouse Stat3 protein fragment containing 155-249 amino acids of Stat3 protein. The invention relates to methods for identifying interacting regions of transcription factors and methods for identifying agents which modulates the interaction between a transcription factor such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for modulating gene transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain
Sequence 95 AA;

```
Query Match      100.0%; Score 477; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 5.9e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
Db 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60

Qy 61 RSIIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
Db 61 RSIIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95

RESULT 2
AAV72852
ID AAY72852 standard; protein; 128 AA.
XX
AC AAY72852;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #10 (155-282 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key
FT Region
FT 24..48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX
PN WO200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023822.
XX
PR 31-AUG-1999; 99US-00387418.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX
PS Claim 65; Page 78; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 155-282
CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX
SQ Sequence 128 AA;
Query Match      100.0%; Score 477; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 8.3e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
Db 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60

Qy 61 RSIIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
Db 61 RSIIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95

Query Match      100.0%; Score 477; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.5e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
Db 49 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 108

Qy 61 RSIIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
Db 109 RSIIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143

RESULT 4
AAV72848
ID AAY72848 standard; protein; 176 AA.
XX
AC AAY72848;
XX
```

```
RESULT 3
AAV72849
ID AAY72849 standard; protein; 143 AA.
XX
AC AAY72849;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #7 (107-249 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key
FT Region
FT 24..48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX
PN WO200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023822.
XX
PR 31-AUG-1999; 99US-00387418.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX
PS Claim 65; Page 75-76; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 107-249
CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX
SQ Sequence 143 AA;
Query Match      100.0%; Score 477; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.5e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
Db 49 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 108

Qy 61 RSIIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
Db 109 RSIIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143

RESULT 4
AAV72848
ID AAY72848 standard; protein; 176 AA.
XX
AC AAY72848;
XX
```

DT 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #6 (107-282 amino acids).
DE
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT Region 24..48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 65; Page 74-75; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-282
XX amino acids of Stat3 protein. The invention relates to methods for
XX identifying interacting regions of transcription factors and methods for
XX identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 176 AA;
Query Match 100.0%; Score 477; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 49 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 108
QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
RESULT 5
AAY72851
ID AAY72851 standard; protein; 213 AA.
XX
AC AAY72851;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 protein fragment #9 (130-342 amino acids).
XX
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.

XX OS Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT Region 1..25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 65; Page 77; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 130-342
XX amino acids of Stat3 protein. This Stat3 fragment showed very weak
XX binding to c-Jun protein in the cell extract. The invention relates to
XX methods for identifying interacting regions of transcription factors and
XX methods for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 213 AA;
Query Match 100.0%; Score 477; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 26 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 85
QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
RESULT 6
AAY72854
ID AAY72854 standard; protein; 223 AA.
XX
AC AAY72854;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 protein fragment #12 (155-377 amino acids).
XX
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
XX Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT Region 188..204
FT /note= "Stat3-c-Jun interaction region 2; corresponds to

FT 342-358 position of Stat3 protein"
 XX WO200116605-A2.
 PN
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 DR
 XX
 XX Identifying an agent for use in modulating the interaction between
 FT transcription factor c-Jun and a Stat3 protein.
 PT
 XX
 PS Claim 65; Page 79; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 protein fragment containing 155-377
 CC amino acids of Stat3 protein. The invention relates to methods for
 CC identifying interacting regions of transcription factors and methods for
 CC identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 CC
 XX Sequence 223 AA;
 SQ
 Query Match 100.0%; Score 477; DB 4; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1.6e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
 DB 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
 QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
 DB 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
 RESULT 7
 AAY72861
 ID AAY72861 standard; protein; 228 AA.
 XX
 AC AAY72861;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 mutant (T346A, K348A, R350A) protein fragment.
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutein.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 213..229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 FT Misc-difference 217
 FT /note= "Wild type Thr substituted with Ala; corresponds
 FT to 346 position of Stat-3 protein"

FT Misc-difference 219
 FT /note= "Wild type Lys substituted with Ala; corresponds
 FT to 348 position of Stat-3 protein"
 FT Misc-difference 221
 FT /note= "Wild type Arg substituted with Ala; corresponds
 FT to 350 position of Stat-3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 DR
 XX
 XX Identifying an agent for use in modulating the interaction between
 FT transcription factor c-Jun and a Stat3 protein.
 PT
 XX
 PS Claim 66; Page 84-85; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 mutant protein fragment containing
 CC 130-358 amino acids of Stat3 protein. This mutant is obtained by
 CC replacing Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the
 CC Stat3 protein. The invention relates to methods for identifying
 CC interacting regions of transcription factors and methods for identifying
 CC agents which modulates the interaction between a transcription factor
 CC such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for
 CC modulating gene transcription e.g., cellular transformation. These
 CC identifying agents are used in the treatment of dysproliferative diseases
 CC and also for treating cancer and psoriasis. A Stat protein comprises the
 CC N-terminal domain, coiled-coil domain, DNA binding domain, linker domain,
 CC SH2 domain and transactivation domain
 CC
 XX Sequence 228 AA;
 SQ
 Query Match 100.0%; Score 477; DB 4; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.6e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
 DB 25 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMR 84
 QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
 DB 85 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 119
 RESULT 8
 AAY72860
 ID AAY72860 standard; protein; 229 AA.
 XX
 AC AAY72860;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 mutant (L148A, V151A, T346A, K348A, R350A) protein fragment.
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutein.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to

```
FT Misc-difference 19 130-154 position of Stat3 protein"
FT /note= "Wild type Leu substituted with Ala; corresponds
FT to 148 position of Stat-3 protein"
FT Misc-difference 22
FT /note= "Wild type Val substituted with Ala corresponds to
FT 151 position of Stat-3 protein"
FT Region
FT 213..229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
FT Misc-difference 217
FT /note= "Wild type Thr substituted with Ala corresponds to
FT 346 position of Stat-3 protein"
FT Misc-difference 219
FT /note= "Wild type Lys substituted with Ala corresponds to
FT 348 position of Stat-3 protein"
FT Misc-difference 221
FT /note= "Wild type Arg substituted with Ala corresponds to
FT 350 position of Stat-3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Example 4; Page; 86pp; English.
XX
XX The present sequence is mouse Stat3 mutant protein fragment containing
XX 130-358 amino acids of Stat3 protein. This mutant is obtained by
XX replacing Leu 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Lys 348
XX with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates
XX to methods for identifying interacting regions of transcription factors
XX and methods for identifying agents which modulates the interaction
XX between a transcription factor such as c-Jun and a Stat protein such as
XX Stat-1 and Stat-3, useful for modulating gene transcription e.g.,
XX cellular transformation. These identifying agents are used in the
XX treatment of dysproliferative diseases and also for treating cancer and
XX psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil
XX domain, DNA binding domain, linker domain, SH2 domain and transactivation
XX domain
XX
XX Sequence 229 AA;
XX
XX Query Match 100.0%; Score 477; DB 4; Length 229;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-40;
XX Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VQDLEQKMKVVENLQDDDFDNFKYTKLSQGDMDLNGNNSVTRQKMQQLTALDQMR 60
XX |||||||
XX 26 VQDLEQKMKVVENLQDDDFDNFKYTKLSQGDMDLNGNNSVTRQKMQQLTALDQMR 85
XX
XX 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
XX |||||||
XX 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
XX
XX RESULT 9
XX AAY72850
XX ID AAY72850 standard; protein; 229 AA.
XX
XX AAY72850;
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```
XX 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #8 (130-358 amino acids).
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX cellular transformation; dysproliferative disease; cancer; psoriasis;
XX therapy.
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Region 1..25
XX /note= "Stat3-c-Jun interaction region 1; corresponds to
XX 130-154 position of Stat3 protein"
XX Region 213..229
XX /note= "Stat3-c-Jun interaction region 2; corresponds to
XX 342-358 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 65; Page 76-77; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 130-358
XX amino acids of Stat3 protein. This Stat3 fragment showed strong binding
XX to c-Jun protein in the cell extract. The invention relates to methods
XX for identifying interacting regions of transcription factors and methods
XX for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 229 AA;
XX
XX Query Match 100.0%; Score 477; DB 4; Length 229;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-40;
XX Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VQDLEQKMKVVENLQDDDFDNFKYTKLSQGDMDLNGNNSVTRQKMQQLTALDQMR 60
XX |||||||
XX 26 VQDLEQKMKVVENLQDDDFDNFKYTKLSQGDMDLNGNNSVTRQKMQQLTALDQMR 85
XX
XX 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
XX |||||||
XX 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
XX
XX RESULT 10
XX AAY72863
XX ID AAY72863 standard; protein; 229 AA.
XX
XX AAY72863;
XX
XX 31-MAY-2001 (first entry)
XX
```

DE Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).

XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; mutein.
XX Mus musculus.

OS
XX
FH Key Location/Qualifiers
FT Region 1..25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
FT Misc-difference 22
FT /note= "Wild type Val substituted with Ala corresponds to
FT 151 position of Stat-3 protein"
FT Region 213..229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
XX
XX
PD 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 66; Page 86; 86pp; English.

XX The present sequence is mouse Stat3 mutant (V151A) protein fragment
CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
CC by replacing Val 151 with Ala in Stat3 protein. The invention relates to
CC methods for identifying interacting regions of transcription factors and
CC methods for identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX
SQ Sequence 229 AA;

Query Match 100.0%; Score 477; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDENYKTLKSGQMDLNGNNQSVTRKMQOQLTALDQMR 60
DB 26 VQDLEQKMKVVENLQDDFDENYKTLKSGQMDLNGNNQSVTRKMQOQLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 11
AA72862
ID AA72862 standard; protein; 229 AA.
XX
AC AA72862;
XX
DT 31-MAY-2001 (first entry)
XX

DE Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).

XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; mutein.
XX Mus musculus.

OS
XX
FH Key Location/Qualifiers
FT Region 1..25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
FT Misc-difference 19
FT /note= "Wild type Leu substituted with Ala; corresponds
FT to 148 position of Stat-3 protein"
FT Region 213..229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
XX
XX
PD 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 66; Page 85; 86pp; English.

XX The present sequence is mouse Stat3 mutant (L148A) protein fragment
CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
CC by replacing Leu 148 with Ala in Stat3 protein. The invention relates to
CC methods for identifying interacting regions of transcription factors and
CC methods for identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX
SQ Sequence 229 AA;

Query Match 100.0%; Score 477; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDENYKTLKSGQMDLNGNNQSVTRKMQOQLTALDQMR 60
DB 26 VQDLEQKMKVVENLQDDFDENYKTLKSGQMDLNGNNQSVTRKMQOQLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 12
AA72847
ID AA72847 standard; protein; 236 AA.
XX
AC AA72847;
XX
DT 31-MAY-2001 (first entry)
XX

XX	Key	Location/Qualifiers	
FT	Region	24. .48	
FT		/note= "Stat3-c-Jun interaction region 1; corresponds to	
FT		130-154 position of Stat3 protein"	
FT	Region	236. .252	
FT		/note= "Stat3-c-Jun interaction region 2; corresponds to	
FT		342-358 position of Stat3 protein"	
XX			
PN	WO200116605-A2.		
XX			
XX	08-MAR-2001.		
XX			
PF	30-AUG-2000; 2000WO-US023822.		
PF			
PR	31-AUG-1999; 99US-00387418.		
XX			
PA	(UTRQ) UNIV ROCKEFELLER.		
XX			
PI	Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;		
XX			
XX	WPI; 2001-226705/23.		
DR			
XX			
PT	Identifying an agent for use in modulating the interaction between		
PT	transcription factor c-Jun and a Stat3 protein.		
XX			
PS	Claim 65; Page 73; 86pp; English.		
XX			
CC	The present sequence is mouse Stat3 protein fragment containing 107-358		
CC	amino acids of Stat3 protein. This Stat3 fragment showed strong binding		
CC	to c-Jun protein in the cell extract. The invention relates to methods		
CC	for identifying interacting regions of transcription factors and methods		
CC	for identifying agents which modulates the interaction between a		
CC	transcription factor such as c-Jun and a Stat protein such as Stat-1 and		
CC	Stat-3, useful for modulating gene transcription e.g., cellular		
CC	transformation. These identifying agents are used in the treatment of		
CC	dysproliferative diseases and also for treating cancer and psoriasis. A		
CC	Stat protein comprises the N-terminal domain, coiled-coil domain, DNA		
CC	binding domain, linker domain, SH2 domain and transactivation domain		
XX			
SQ	Sequence 252 AA;		
Query Match			
Best Local Similarity 100.0%; Score 477; DB 4; Length 252;			
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
Qy	1	VQLEQRMKVVENLQDDFDNFNTKLKSGQDMQDLNGNNQSVTRQMQQLQMLTALDQMR 60	
Db	49	VQLEQRMKVVENLQDDFDNFNTKLKSGQDMQDLNGNNQSVTRQMQQLQMLTALDQMR 100	
Qy	61	RSIVSELAGLLSAMEYVQKLTLDLELADWKRPEI 95	
Db	109	RSIVSELAGLLSAMEYVQKLTLDLELADWKRPEI 143	
RESULT 14			
AAAY72841			
ID	AAAY72841	standard; protein; 271 AA.	
XX			
AC	AAAY72841;		
XX			
DT	31-MAY-2001	(first entry)	
XX			
DE	Mouse Stat3 protein fragment #2 (107-377 amino acids).		
XX			
KW	Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;		
KW	cellular transformation; dysproliferative disease; cancer; psoriasis;		
KW	therapy.		
XX			
OS	Mus musculus.		
XX			
Key	Location/Qualifiers		
FT	Region	24. .48	

FT FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT PT 130-154 position of Stat3 protein"
 FT PT 236..252
 FT PT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT PT 342-358 position of Stat3 protein"
 FT XX
 PN WO200116605-A2.
 XX
 XX 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 PI WPI; 2001-226705/23.
 DR
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 PT
 XX Claim 65; Page 67-68; 86pp; English.
 PS
 XX The present sequence is mouse Stat3 protein fragment containing 107-377
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 271 AA;
 Query Match 100.0%; Score 477; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLTALDQMR 60
 DB 49 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLTALDQMR 108
 QY 61 RSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 95
 DB 109 RSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 143
 RESULT 15
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX
 AC AAR72082;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX
 DE Mouse Stat3 (19sf6).
 XX
 KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX
 OS Mus sp.
 XX
 PN WO9508629-A1.
 XX
 PD 30-MAR-1995.
 XX

PF 26-SEP-1994; 94WO-US010849.
 XX
 PR 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126595.
 PR 11-MAR-1994; 94US-00212184.
 PR 11-MAR-1994; 94US-00212185.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 PI WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 XX
 PT Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX
 XX Claim 1; Page 107-110; 160pp; English.
 XX
 XX A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;
 Query Match 100.0%; Score 477; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.8e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLTALDQMR 60
 DB 155 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLTALDQMR 214
 QY 61 RSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 95
 DB 215 RSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 249
 Search completed: May 25, 2005, 17:36:34
 Job time : 58.7327 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 11.8868 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-21
Perfect score: 477
Sequence: 1 VQDLEQMKVVENLQDDDF...YVQKLTDEELADWKRPEI 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	95	US-09-387-418A-21	Sequence 21, Appl
2	477	100.0	128	US-09-387-418A-20	Sequence 20, Appl
3	477	100.0	143	US-09-387-418A-17	Sequence 17, Appl
4	477	100.0	176	US-09-387-418A-16	Sequence 16, Appl
5	477	100.0	213	US-09-387-418A-19	Sequence 19, Appl
6	477	100.0	223	US-09-387-418A-22	Sequence 22, Appl
7	477	100.0	229	US-09-387-418A-18	Sequence 28, Appl
8	477	100.0	229	US-09-387-418A-28	Sequence 28, Appl
9	477	100.0	229	US-09-387-418A-29	Sequence 29, Appl
10	477	100.0	229	US-09-387-418A-30	Sequence 30, Appl
11	477	100.0	229	US-09-387-418A-31	Sequence 31, Appl
12	477	100.0	236	US-09-387-418A-15	Sequence 15, Appl
13	477	100.0	252	US-09-387-418A-14	Sequence 14, Appl
14	477	100.0	271	US-09-387-418A-9	Sequence 9, Appl
15	477	100.0	770	US-08-369-796-12	Sequence 12, Appl
16	477	100.0	770	US-08-852-091-12	Sequence 12, Appl
17	477	100.0	770	US-08-820-754-12	Sequence 12, Appl
18	477	100.0	770	US-08-956-652-12	Sequence 12, Appl
19	477	100.0	770	US-08-956-869-12	Sequence 12, Appl
20	477	100.0	770	US-08-948-547-12	Sequence 12, Appl
21	477	100.0	770	US-09-364-970-3	Sequence 3, Appl
22	477	100.0	770	US-09-364-970-5	Sequence 5, Appl
23	477	100.0	770	US-08-956-653A-12	Sequence 12, Appl
24	477	100.0	770	US-08-212-185-12	Sequence 12, Appl
25	477	100.0	770	PCT-US95-17025-12	Sequence 12, Appl
26	466	97.7	770	US-08-416-581B-1	Sequence 1, Appl
27	466	97.7	770	US-08-416-581B-5	Sequence 5, Appl

28	466	97.7	770	1	US-08-416-581B-9	Sequence 9, Appl
29	466	97.7	770	3	US-09-012-710-8	Sequence 8, Appl
30	466	97.7	770	3	US-09-087-465-6	Sequence 6, Appl
31	466	97.7	770	3	US-09-556-273-8	Sequence 8, Appl
32	466	97.7	770	3	US-09-526-542-2	Sequence 2, Appl
33	466	97.7	770	4	US-09-972-800A-6	Sequence 6, Appl
34	466	97.7	770	4	US-10-117-087-2	Sequence 2, Appl
35	466	97.7	771	1	US-08-276-099A-14	Sequence 14, Appl
36	466	97.7	771	1	US-08-781-890-14	Sequence 14, Appl
37	278	58.3	185	3	US-09-387-418A-23	Sequence 23, Appl
38	173	36.3	748	1	US-08-408-318-2	Sequence 2, Appl
39	173	36.3	748	1	US-08-839-164-2	Sequence 2, Appl
40	173	36.3	748	3	US-09-087-465-8	Sequence 8, Appl
41	173	36.3	748	4	US-09-972-800A-8	Sequence 8, Appl
42	170	35.6	749	1	US-08-369-796-8	Sequence 8, Appl
43	170	35.6	749	2	US-08-852-091-8	Sequence 8, Appl
44	170	35.6	749	2	US-08-820-754-8	Sequence 8, Appl
45	170	35.6	749	3	US-08-956-652-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-387-418A-21
; Sequence 21, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-21

Query Match	100.0%	Score 477;	DB 3;	Length 95;
Best Local Similarity	100.0%	Pred. No. 3.8e-45;	Mismatches 0;	Indels 0;
Matches	95;	Conservative	0;	Gaps 0;
QY	1	VQDLEQMKVVENLQDDDFDNFKTLKSQGDMDLNGNNSVTRQKMQQLQEQMLTALDQMR	60	
Db	1	VQDLEQMKVVENLQDDDFDNFKTLKSQGDMDLNGNNSVTRQKMQQLQEQMLTALDQMR	60	
QY	61	RSIVSELGLLSAMEYVQKLTDEELADWKRPEI	95	
Db	61	RSIVSELGLLSAMEYVQKLTDEELADWKRPEI	95	

RESULT 2
US-09-387-418A-20
; Sequence 20, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-20

Query Match      100.0%; Score 477; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.5e-45;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||||||
Db 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||||||

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||||||
Db 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||||||

RESULT 3
US-09-387-418A-17
; Sequence 17, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-17

Query Match      100.0%; Score 477; DB 3; Length 143;
Best Local Similarity 100.0%; Pred. No. 6.4e-45;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||||||
Db 49 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 108
    |||||||

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||||||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
    |||||||

RESULT 4
US-09-387-418A-16
; Sequence 16, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 176
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-16

Query Match      100.0%; Score 477; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 8.2e-45;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||||||
Db 49 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 108
    |||||||

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||||||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
    |||||||

RESULT 5
US-09-387-418A-19
; Sequence 19, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-19

Query Match      100.0%; Score 477; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||||||
Db 26 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 85
    |||||||

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||||||
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
    |||||||

RESULT 6
US-09-387-418A-22
; Sequence 22, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-22
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Query Match      100.0%; Score 477; DB 3; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

RESULT 7
US-09-387-418A-18
; Sequence 18, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-18

Query Match      100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 26 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 8
US-09-387-418A-28
; Sequence 28, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-28

Query Match      100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
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```
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 26 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 9
US-09-387-418A-29
; Sequence 29, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-29

Query Match      100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 26 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 10
US-09-387-418A-30
; Sequence 30, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-30

Query Match      100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 26 VQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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Db	26	VQDLEQWKVYENLQDDFFNYATLKSQGMODLGNNGSVTRQKMQQLQEQMLTALDQMR	85
Qy	61	RSIVSELAGLLSMEYVQKLTLTDEELADWKRRPEI	95
Db	86	RSIVSELAGLLSMEYVQKLTLTDEELADWKRRPEI	120

RESULT 11
US-09-387-418A-31
; Sequence 31, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-31

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Best Local Similarity	100.0%;	Pred. No. 1.1e-44;		
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RESULT 12
US-09-387-418A-15
; Sequence 15, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-15

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Db	49	VQDLEKMKVVENLQDDFD	FNYKTLKSGQDMQDLGNNGNS	VTRQKMOOLEMLTALDQMR	108

Qy 61 RSIYSELAGLISAMEYVQKTLTDEELADWKRPEI 95
| | | | | | | | | | | | | | | | | | | | | |
pb 109 RSIYSELAGLISAMEYVQKTLTDEELADWKRPEI 143

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RESULT 13
US-09-387-418A-14
; Sequence 14, Application US/09387418A
; Patent NO. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-14

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Qy	61	RSIVSELAGLISAMEYVOKTLTDEELADWKKRPEI	95	
Db	109	RSIVSELAGLISAMEYVOKTLTDEELADWKKRPEI	143	

RESULT 14
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match	100.0%	Score 477;	DB 3;	Length 271;
Best Local Similarity	100.0%;	Pred. No. 1.4e-44;		
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QY	61	RSIVSELAGLISAMEYVQKTLTDEELADWKRPEI	95	
Db	109	RSIVSELAGLISAMEYVQKTLTDEELADWKRPEI	143	

RESULT 15
 US-08-369-796-12
 ; Sequence 12, Application US/08369796
 ; Patent No. 5716622
 ; GENERAL INFORMATION:
 ; APPLICANT: James E. Darnell, Jr.
 ; APPLICANT: Zilong Wen
 ; APPLICANT: Curt M. Horvath
 ; APPLICANT: Zhong Zhong
 ; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 ; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/369,796
 ; FILING DATE: 06-JAN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-369-796-12

Query Match 100.0%; Score 477; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.1e-44;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 155 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNGSVTRQKMQQLTALDQMR 214
 QY 61 RSIVSELGLLSAMEYVQKTLTDEELADWKRRPEI 95
 DB 215 RSIVSELGLLSAMEYVQKTLTDEELADWKRRPEI 249

Search completed: May 25, 2005, 17:47:37
 Job time : 15.8868 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:36:58 ; Search time 41.6038 Seconds
(without alignments)
763.830 Million cell updates/sec

Title: US-10-090-185-21
Perfect score: 477
Sequence: 1 VQDLEQKMKVENVLQDDFDF.....YVQKTLTDEELADWKRPEI 95

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Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	100.0	95	US-10-090-185-21	Sequence 21, Appl
2	477	100.0	128	US-10-090-185-20	Sequence 20, Appl
3	477	100.0	143	US-10-090-185-17	Sequence 17, Appl
4	477	100.0	176	US-10-090-185-16	Sequence 16, Appl
5	477	100.0	213	US-10-090-185-19	Sequence 19, Appl
6	477	100.0	223	US-10-090-185-22	Sequence 22, Appl
7	477	100.0	229	US-10-090-185-18	Sequence 18, Appl
8	477	100.0	229	US-10-090-185-28	Sequence 28, Appl
9	477	100.0	229	US-10-090-185-29	Sequence 29, Appl
10	477	100.0	229	US-10-090-185-30	Sequence 30, Appl
11	477	100.0	229	US-10-090-185-31	Sequence 31, Appl
12	477	100.0	236	US-10-090-185-15	Sequence 15, Appl
13	477	100.0	252	US-10-090-185-14	Sequence 14, Appl

14	477	100.0	271	13	US-10-090-185-9	Sequence 9, Appli
15	477	100.0	770	11	US-09-876-773-12	Sequence 12, Appl
16	477	100.0	770	17	US-10-639-617-12	Sequence 12, Appl
17	466	97.7	720	15	US-10-380-020-4	Sequence 4, Appli
18	466	97.7	769	15	US-10-380-020-2	Sequence 2, Appli
19	466	97.7	769	15	US-10-380-020-5	Sequence 5, Appli
20	466	97.7	770	14	US-10-045-792-8	Sequence 8, Appli
21	466	97.7	770	14	US-10-038-010-56	Sequence 56, Appl
22	466	97.7	770	14	US-10-117-087-2	Sequence 2, Appli
23	466	97.7	770	15	US-10-116-275-329	Sequence 329, App
24	466	97.7	770	15	US-10-116-275-349	Sequence 349, App
25	466	97.7	793	9	US-09-925-302-780	Sequence 780, App
26	466	97.7	793	10	US-09-925-302-780	Sequence 23, Appl
27	278	58.3	185	13	US-10-090-185-23	Sequence 437, App
28	173	36.3	423	14	US-10-177-293-437	Sequence 439, App
29	173	36.3	748	14	US-10-177-293-439	Sequence 70, Appl
30	173	36.3	748	16	US-10-755-889-70	Sequence 362, App
31	173	36.3	748	16	US-10-755-889-362	Sequence 6, Appli
32	170	35.6	749	9	US-09-833-205-6	Sequence 8, Appli
33	170	35.6	749	11	US-09-876-773-8	Sequence 8, Appli
34	170	35.6	749	14	US-10-045-792-7	Sequence 7, Appli
35	170	35.6	749	14	US-10-205-194-39	Sequence 39, Appl
36	170	35.6	749	17	US-10-639-617-8	Sequence 8, Appli
37	168	35.2	749	9	US-09-833-205-4	Sequence 4, Appli
38	160.5	33.6	749	14	US-10-045-792-9	Sequence 9, Appli
39	158	33.1	268	13	US-10-090-185-12	Sequence 12, Appl
40	158	33.1	582	14	US-10-245-120-3	Sequence 3, Appli
41	158	33.1	712	11	US-09-876-773-6	Sequence 6, Appli
42	158	33.1	712	14	US-10-245-120-2	Sequence 2, Appli
43	158	33.1	712	17	US-10-639-617-6	Sequence 6, Appli
44	158	33.1	712	17	US-10-639-617-6	Sequence 5, Appli
45	158	33.1	750	9	US-09-833-205-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-090-185-21
; Sequence 21, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 21
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-21

Query Match 100.0%; Score 477; DB 13; Length 95;

Best Local Similarity 100.0%; Pred. No. 1.8e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVENVLQDDFDFNYKTLKSGQDMQDLNGNSVTRQKQQLTALDQMR 60
DB 1 VQDLEQKMKVENVLQDDFDFNYKTLKSGQDMQDLNGNSVTRQKQQLTALDQMR 60

QY 61 RSTVSELGALLSAMEYVQKTLTDEELADWKRPEI 95

DB 61 RSTVSELGALLSAMEYVQKTLTDEELADWKRPEI 95

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RESULT 2
US-10-090-185-20
; Sequence 20, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-20

Query Match      100.0%; Score 477; DB 13; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VQLEQKMKVVENLQDDFDENYKTLKSGQDMQDLNGNNSQSVTRKMQQLEQMLTALDQMR 60

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

RESULT 3
US-10-090-185-17
; Sequence 17, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-17

Query Match      100.0%; Score 477; DB 13; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 49 VQLEQKMKVVENLQDDFDENYKTLKSGQDMQDLNGNNSQSVTRKMQQLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
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RESULT 4
US-10-090-185-16
; Sequence 16, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-16

Query Match      100.0%; Score 477; DB 13; Length 176;
Best Local Similarity 100.0%; Pred. No. 3.8e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 49 VQLEQKMKVVENLQDDFDENYKTLKSGQDMQDLNGNNSQSVTRKMQQLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143

RESULT 5
US-10-090-185-19
; Sequence 19, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-19

Query Match      100.0%; Score 477; DB 13; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.8e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 26 VQLEQKMKVVENLQDDFDENYKTLKSGQDMQDLNGNNSQSVTRKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
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Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 6

US-10-090-185-22

; Sequence 22, Application US/10090185

; Publication No. US20020197647A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/10/090,185

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: 09/387,418

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 22

; LENGTH: 223

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-090-185-22

Query Match 100.0%; Score 477; DB 13; Length 223;

Best Local Similarity 100.0%; Pred. No. 5.1e-42;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

RESULT 7

US-10-090-185-18

; Sequence 18, Application US/10090185

; Publication No. US20020197647A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/10/090,185

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: 09/387,418

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-090-185-18

Query Match 100.0%; Score 477; DB 13; Length 229;

Best Local Similarity 100.0%; Pred. No. 5.3e-42;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60

Db 26 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 8

US-10-090-185-28

; Sequence 28, Application US/10090185

; Publication No. US20020197647A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/10/090,185

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: 09/387,418

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 28

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-090-185-28

Query Match 100.0%; Score 477; DB 13; Length 229;

Best Local Similarity 100.0%; Pred. No. 5.3e-42;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60

Db 26 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 9

US-10-090-185-29

; Sequence 29, Application US/10090185

; Publication No. US20020197647A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/10/090,185

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: 09/387,418

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 29

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-090-185-29

Query Match 100.0%; Score 477; DB 13; Length 229;

Best Local Similarity 100.0%; Pred. No. 5.3e-42;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 60

Db 26 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 10

US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-30

Query Match 100.0%; Score 477; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMDLNGNNSVTRQKMOQLTALDQMR 60
Db 26 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMDLNGNNSVTRQKMOQLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 11

US-10-090-185-31
; Sequence 31, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-31

Query Match 100.0%; Score 477; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMDLNGNNSVTRQKMOQLTALDQMR 60
Db 26 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMDLNGNNSVTRQKMOQLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 12

US-10-090-185-15
; Sequence 15, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-15

Query Match 100.0%; Score 477; DB 13; Length 236;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMDLNGNNSVTRQKMOQLTALDQMR 60
Db 49 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMDLNGNNSVTRQKMOQLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143

RESULT 13

US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 100.0%; Score 477; DB 13; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.9e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGDMDLNGNNSVTRQKMOQLTALDQMR 60
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143

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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO 993/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match      100.0%; Score 477; DB 11; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY    1 VQDLEOKMKVVENLQDDFDENFKYTKLSQGMDLNGNNQSVTROKMQOLEQMLTALDOMR 60
Db    155 VQDLEQRKMKVVENLQDDFDENFKYTKLSQGMDLNGNNQSVTROKMQOLEQMLTALDOMR 214

QY    61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db    215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249

Search completed: May 25, 2005, 18:21:48
Job time : 53.9371 secs

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Search completed: May 25, 2005, 18:21:48
Job time : 53.9371 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 8.96226 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-21
Perfect score: 477
Sequence: 1 VQDLQKMKVVENLQDDFD.....YVQKTLTDELDADWKRPEI 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	97.7	770	2 A54444	DNA-binding protei
2	466	97.7	770	2 I49508	ISGF3 p91-related
3	164	34.4	748	2 A56047	gamma-interferon a
4	158	33.1	739	2 A46159	interferon-depende
5	93	19.5	786	2 I49274	mammary gland fact
6	93	19.5	793	2 S54772	mammary gland fact
7	89	18.7	794	2 G02317	transcription acti
8	88	18.4	794	2 S55227	mammary gland fact
9	86	18.0	533	2 G72593	hypothetical prote
10	85.5	17.9	2094	2 S33124	tpr protein - huma
11	84.5	17.7	217	2 G75219	hypothetical prote
12	84.5	17.7	821	2 T24728	hypothetical prote
13	83.5	17.5	3187	2 JCS537	364K Golgi complex
14	82	17.2	1818	1 S73852	hypothetical prote
15	81.5	17.1	217	2 B71203	hypothetical prote
16	79.5	16.7	278	2 AC3354	hypothetical prote
17	79	16.6	638	2 S67605	hypothetical prote
18	78	16.4	1968	1 S05697	myosin heavy chain
19	77.5	16.2	1160	2 I40589	parasporal crystal
20	77	16.1	304	2 AD1029	probable membrane
21	77	16.1	569	2 B71902	hypothetical prote
22	76.5	16.0	441	2 T01613	hypothetical prote
23	76	15.9	821	2 S67087	hypothetical prote
24	75.5	15.8	734	2 T27055	hypothetical prote
25	75.5	15.8	1085	2 F96712	hypothetical prote
26	75	15.7	742	1 S86591	kinesin-related pr
27	75	15.7	750	2 T38435	coiled coil protei
28	75	15.7	896	2 T43074	epidermal growth f
29	75	15.7	1171	2 T45706	chromosome-associa

30	74.5	15.6	1979	1 S03166	myosin heavy chain
31	74	15.5	412	2 S07537	myosin heavy chain
32	74	15.5	621	2 S10450	myosin heavy chain
33	73.5	15.4	398	2 AC1763	peptidoglycan lyti
34	73.5	15.4	927	2 AG1739	transmembrane prot
35	73.5	15.4	980	2 E71606	hypothetical prote
36	73	15.3	764	2 I51302	myosin heavy chain
37	73	15.3	1526	2 T41522	myosin ii - fisio
38	73	15.3	1738	2 T14867	interaprin - slime
39	72.5	15.2	986	2 T10754	cis-Golgi matrix p
40	72.5	15.2	1046	2 T42734	cytoplasmic linker
41	72.5	15.2	1133	2 T22976	hypothetical prote
42	72.5	15.2	2024	2 A54103	centrosome autoant
43	72	15.1	173	2 JCS610	tropinin I - sea s
44	72	15.1	262	2 JC1237	apolipoprotein A-I
45	72	15.1	264	2 S22420	apolipoprotein A-I

ALIGNMENTS

RESULT 1

A54444
DNA-binding protein APRP - human
C:Species: Homo sapiens (man)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: A54444
R:Akita, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A>Title: Molecular cloning of APRP, a novel IFN-stimulated gene factor 3 p91-related tr
A:Reference number: A54444; MUID:94208062; PMID:7512451
A:Accession: A54444
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-770 <RES>
A:Cross-references: UNIPROT:P40763; GB:L29277; NID:9475788; PID:9475789
C:Genetics:
A:Gene: GDB:STAT3; APRF
A:Cross-references: GDB:358950
A:Map position: 17q21-17q21
A:Superfamily: human signal transducer and transcription activator STAT5A
C:Keywords: DNA binding; transcription factor

Query Match 97.7%; Score 466; DB 2; Length 770;
Best Local Similarity 97.9%; Pred. No. 1.3e-31;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VQDLQKMKVVENLQDDFDPNYKTLKSGQMDLNGNQSVTQRKMQQLTALDOMR 60
Db 155 VQDLQKMKVVENLQDDFDPNYKTLKSGQMDLNGNQSVTQRKMQQLTALDOMR 214

Qy 61 RSTVSELGALLSAMEYVQKTLTDELDADWKRPEI 95
Db 215 RSTVSELGALLSAMEYVQKTLTDELDADWKRPEI 249

RESULT 2

I49508

ISGF3 p91-related transcription factor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49508; I49009

R:Akita, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matusaka, T.; Yoshida, K.; Su

Cell 77, 63-71, 1994

A>Title: Molecular cloning of APRP, a novel IFN-stimulated gene factor 3 p91-related tr

A:Reference number: A54444; MUID:94208062; PMID:7512451

A:Accession: I49508

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-770 <RES>

A:Cross-references: UNIPROT:P42227; GB:L29278; NID:9476715; PID:AAA37254.1; PID:947671

R:Raz, R.; Durbin, J.E.; Levy, D.E.

J. Biol. Chem. 269, 24391-24395, 1994

A>Title: Acute phase response factor and additional members of the interferon-stimulated
A/Reference number: I49009; MUID:95014185; PMID:7523373
A/Accession: I49009
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-393, 'M', 395-700, 702-770 <RE2>
A/Cross-references: EMBL:U08378; NID:9473889; PIDN:AAA5668.1; PID:9473890
C/Genetics:
C/Supfamily: human signal transducer and transcription activator STAT5A

Query Match 97.7%; Score 466; DB 2; Length 770;
Best Local Similarity 97.9%; Pred. No. 1.3e-31;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQMR 60
DB 155 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQMR 214
QY 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 215 RSIVSELAGLLSMEYVQKTLTDEELADWKRRQOI 249

RESULT 3
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: A56047
R/Tamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, M.; Cell. Biol. 14, 4342-4349, 1994
A/Title: Stat4, a novel gamma interferon activation site-binding protein expressed in ea
A/Reference number: A56047; MUID:94277038; PMID:8007943
A/Accession: A56047
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-748 <YAM>
A/Cross-references: UNIPROT:P42228; GB:U09351; NID:9509502; PIDN:AAA19692.1; PID:9509503
C/Supfamily: human signal transducer and transcription activator STAT5A
C/Keywords: DNA binding; phosphoprotein

Query Match 34.4%; Score 164; DB 2; Length 748;
Best Local Similarity 35.1%; Pred. No. 2.8e-06;
Matches 34; Conservative 26; Mismatches 29; Indels 8; Gaps 2;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQ 58
DB 154 VQTEQDTKYLEDLQDEFDYRYKTIQTMQDQ-----KNSILVQEVLTILQEMLSLDF 207

QY 59 MRSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 208 KRKEALSKMTQIVNETDLNMSLLEELQDWKRRQOI 244

RESULT 4
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C/Species: Homo sapiens (man)
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A46159
R/Schindler, C.; Fu, X.Y.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 7836-7839, 1992
A/Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
A/Reference number: A46159; MUID:92366557; PMID:1502203
A/Accession: A46159
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid; protein
A/Residues: 1-739 <SCH>
A/Cross-references: UNIPROT:P42224
A/Experimental source: HeLa cells
A/Note: sequence extracted from NCBI backbone (NCBIP:110818)
C/Supfamily: human signal transducer and transcription activator STAT5A

Query Match 33.1%; Score 158; DB 2; Length 739;
Best Local Similarity 36.2%; Pred. No. 8.9e-06;
Matches 34; Conservative 22; Mismatches 36; Indels 2; Gaps 1;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQMR 60
DB 153 VMCIEHEIKSLBQLQDEYDFKCKTL--QNRHETNGVAKSDQKQBQLLLKKMYLLMDNKR 210
QY 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 94
DB 211 KEVHKIITELNVTTELTONALINDELVEVKRRQQ 244

RESULT 5
I49274
mammary gland factor - mouse
N/Alternate names: STAT5 protein homolog p80
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I49274; S54773; S54727
R/Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A/Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved
A/Reference number: I49273; MUID:96004632; PMID:7568026
A/Accession: I49274
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-786 <RES>
A/Cross-references: UNIPROT:P42232; UNIPROT:Q9JYK1; EMBL:U21110; NID:9747973; PIDN:AACS
R/Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A/Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A/Reference number: S54772; MUID:95237158; PMID:7720707
A/Accession: S54773
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-432, 'E', 434-786 <MUI>
A/Cross-references: EMBL:Z48539; NID:9758635; PIDN:CAA88420.1; PID:9758636
R/Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A/Title: Interleukin-3 signals through multiple isoforms of Stat5.
A/Reference number: S54725; MUID:95246733; PMID:7537213
A/Accession: S54727
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-432, 'E', 434-786 <AZA>
C/Genetics:
A/Gene: Stat5b
C/Supfamily: human signal transducer and transcription activator STAT5A

Query Match 19.5%; Score 93; DB 2; Length 786;
Best Local Similarity 26.4%; Pred. No. 2.7;
Matches 28; Conservative 18; Mismatches 48; Indels 12; Gaps 3;

QY 2 QDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQMR 53
DB 156 QDTENELKKLQQTQYEFIIQYQESLRTQAFQALGQLNPQBRMSRETALQKQVSLTTL 215
QY 54 -----TALDQMRRSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 216 QREAQTLQYRVVELAEKHQKTLQLLRQKQTLILDELIQWKRQOL 261

RESULT 6
S54772
mammary gland factor - mouse
N/Alternate names: stat5 protein
C/Species: Mus musculus (house mouse)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S54772; I49273
R/Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-793 <MUI>
A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIA0; EMBL:Z48538; NID:g758633; PIDN:CAA88
R;Lin, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stats and an additional homologue (Stat5b) involved in
A;Reference number: I49273; MUID:96004632; PMID:7568026
A;Accession: I49273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-793 <RES>
A;Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972
C;Genetics:
A;Gene: Stat5a
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 19.5%; Score 93; DB 2; Length 793;
Best Local Similarity 26.4%; Pred. No. 2.7;
Matches 28; Conservative 18; Mismatches 48; Indels 12; Gaps 3;

QY 2 QDLEQKQKVVENLQDDFDNY-KTLKSGQDMQDLNGNN-----OSVTRKMQQLEQML 53
DB 156 QDTNELKKLQQTQEQYFIITQYQESLRQAQFAQLAQLNPOERLSRETALQQKQVSLAWL 215

QY 54 ----TALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 216 QREAQTLQYRVVELAEKHQKTLQLLRKQQTIIILDDDELQWKRQQL 261

RESULT 7
G02317
transcription activator stat5a - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
R;Lin, J.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:gl151169; PIDN:AA806589.1; PID:gl15
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 18.7%; Score 89; DB 2; Length 794;
Best Local Similarity 25.5%; Pred. No. 6;
Matches 27; Conservative 19; Mismatches 48; Indels 12; Gaps 3;

QY 2 QDLEQKQKVVENLQDDFDNY-KTLKSGQDMQDL-----NGNQSVTRKMQQLEQML 53
DB 156 QDTNELKKLQQTQEQYFIITQYQESLRQAQFAQLAQLNPOERLSRETALQQKQVSLAWL 215

QY 54 ----TALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 216 QREAQTLQYRVVELAEKHQKTLQLLRKQQTIIILDDDELQWKRQQL 261

RESULT 8
S55527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: S55527; MUID:95188889; PMID:7882987
A;Accession: S55527

A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g602
A;Note: this is a revision to the sequence from reference S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcr
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716, 'RHLGPGSLPSR', 729, 'P', 731, 'ASL', <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 18.4%; Score 88; DB 2; Length 794;
Best Local Similarity 27.2%; Pred. No. 7.2;
Matches 28; Conservative 16; Mismatches 47; Indels 12; Gaps 3;

QY 2 QDLEQKQKVVENLQDDFDNY-KTLKSGQDMQDLNGNN-----OSVTRKMQQLEQML 53
DB 157 QDTNELKKLQQTQEQYFIITQYQESLRQAQFAQLAQLNPOERLSRETALQQKQVSLAWL 216

QY 54 ----TALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 92
DB 217 QREAQTLQYRVVELAEKHQKTLQLLRKQQTIIILDDDELQWKR 259

RESULT 9
G72593
hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72593
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-533 <NAW>
A;Cross-references: UNIPROT:Q9YCP2; DBJ:AP000061; NID:gs104821; PIDN:BA80205.1; PID:d
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1216

Query Match 18.0%; Score 86; DB 2; Length 533;
Best Local Similarity 22.5%; Pred. No. 6.9;
Matches 23; Conservative 27; Mismatches 32; Indels 20; Gaps 3;

QY 1 VQDLQKQKVVEN---LQDDF-----DFNYKTLKSGQDMQDLNGNQSV 41
DB 337 VEDLEARVGSVDRLSQAEEIDSLTSLDSLTETLELDSLRLAEQAQSLIEDLTRLDDQV 396

QY 42 TRQKMQQLEQMLTALDQWRRSIVSELAGLLSAMEYVQKTLTD 83
DB 397 A-STLQQLQORLATAEESLQALTEDLASLQAEVETLQQSIVE 437

RESULT 10
S33124
tpr protein - human
N;Alternate names: kinase-related transforming protein (tpr-met); protein with promoter
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S33124; S23740; S00928; G01185
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2329-2333, 1992
A;Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive co
A;Reference number: S33124; MUID:93064711; PMID:1437155
A;Accession: S33124

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2094 <MIT>
A;Cross-references: UNIPROT:Q15624; UNIPROT:Q9UE33; EMBL:X66397; NID:g633225
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 383-388, 1992
A;Title: Nucleotide sequence analysis of human tpr cDNA clones.
A;Reference number: S23740; MUID:92195670; PMID:1549355
A;Accession: S23740
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-725, 'L' <MI2>
A;Cross-references: EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID:g37258
R;King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
Oncogene 2, 617-619, 1988
A;Title: Tpr homologues activate met and raf.
A;Reference number: S00928; MUID:88262257; PMID:3387099
A;Accession: S00928
A;Molecule type: mRNA
A;Residues: 1-31, 'R', 33-142 <KIN>
A;Cross-references: EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID:g37256
R;Greco, A.
submitted to the EMBL Data Library, December 1995
A;Reference number: H00592
A;Accession: G01185
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 144-228 <GRE>
A;Cross-references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798
C;Genetics:
A;Gene: GDB:TPR
A;Cross-references: GDB:l128821; OMIM:189940
A;Map position: 1q25-1q25
A;Introns: 177/3

Query Match 17.9%; Score 85.5; DB 2; Length 2094;
Best Local Similarity 26.5%; Pred. No. 33;
Matches 26; Conservative 24; Mismatches 21; Indels 27; Gaps 4;

QY 3 DLQKMKV---VENLQDDFDNFYKTLKSKQ-----GDMQDLNGNNSVTRQKMQ 47
DB 1423 DLQKVKITQVKKIGRRYQTVQEEKKAQDKVMETSQAQSSGDHQE-----QHVSVQEMQ 1477

QY 48 QLEQMLTALDQMRSSIVSELAGLLSAMEYVQKLTDEE 85
DB 1478 ELKETLNQAEKTKSKLSLSQ-----VENLQKTLSEKE 1508

RESULT 11

G75219
hypothetical protein PAB2166 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G75219
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: G75219
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <KAW>
A;Cross-references: UNIPROT:Q9W122; GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CA84920
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB2166

Query Match 17.7%; Score 84.5; DB 2; Length 217;
Best Local Similarity 24.0%; Pred. No. 3.6;
Matches 23; Conservative 31; Mismatches 31; Indels 11; Gaps 3;

QY 1 VQDLEQKMKVVENLQDDFD-FNYKTLKSGDMQDLNGNNSVTRQKMOOLEQMLTALDQM 59

DB 132 LLELKRKVRLEVLDEDFHLKEQLIKQEGQLE-----MAREYIKLLEGVRHIDNI 183
QY 60 RRSIVSELAGLLSAMEYVQKLTDEELADMKRPEI 95
DB 184 KANVTLLSGYLE--DVIRKIVNDELNARGLKRTPI 217

RESULT 12

T24728
hypothetical protein T09A5.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24728
R;Lightning, J.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19928
A;Accession: T24728
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-821 <WIL>
A;Cross-references: UNIPROT:P45970; EMBL:Z36753; PIDN:CAA85342.1; GSPDB:GNO0020; CESP:T
A;Experimental source: clone T09A5
C;Genetics:
A;Gene: CESP:T09A5.10
A;Map position: 2
A;Introns: 47/2; 253/2; 604/3; 643/1; 712/3

Query Match 17.7%; Score 84.5; DB 2; Length 821;
Best Local Similarity 23.9%; Pred. No. 15;
Matches 27; Conservative 22; Mismatches 31; Indels 33; Gaps 3;

QY 2 ODLEQKMKVVENLQDDFDNFYKTLKSGDMQDLNG-----NNQSVTRQKMQ 47
DB 318 ENLTAKLKTVT-----EDNGKMKQARELDNDYEFARFROEQEQLTTLRATQDMA 371

QY 48 QLEQMLTALDQMRSSIVSELAGLLSAMEYV-----OKLTDELA 87
DB 372 DLQELTGVEKIRASLKSENESSLASVEELSVASLRNKQADNSKTMLSELA 424

RESULT 13

JC5837
364K Golgi complex-associated protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JC5837
R;Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Y.
Cell Struct. Funct. 22, 565-577, 1997
A;Title: Identification and characterization of rat 364-kDa Golgi-associated protein re
A;Reference number: JC5837; MUID:98093490; PMID:9431462
A;Accession: JC5837
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-3187 <ROK>
A;Cross-references: UNIPROT:Q63714; DBJ:D25543; NID:D25543; PIDN:BAA05026.1; PID:g516
C;Comment: This protein plays a role in the formation and maintenance of the characteri
C;Superfamily: Gintin
F;49-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status predic
F;3165-3187/Domain: membrane anchor #status predicted <MAD>

Query Match 17.5%; Score 83.5; DB 2; Length 3187;
Best Local Similarity 25.5%; Pred. No. 76;
Matches 26; Conservative 17; Mismatches 40; Indels 19; Gaps 2;

QY 3 DLEQKMKVVENLQDDFDNFYKTLKSGDMQDLNGNNSVTRQKMOOLEQMLTALDQ----- 58
DB 150 ELQEKELISNLOAQDLQAOSEQASOLDKSAEMEDFILMRQKLOEKKEELIGALQOTLSQ 209

QY 59 -----MERSIVSE---LAGLLSAMEYVQKLTDEE 85

DB 210 TQAEQAQKURVMORKLEEHEALLGRAQVVDLLQKELTSAE 251

REF ID: A673852

Search completed: May 25, 2005, 17:45:23
Job time : 12.9623 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 39.5283 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-21

Perfect score: 477

Sequence: 1 VQDLQKMKVENLQDDDF.....YVQKTLTDELADWKRPEI 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	466	97.7	770	1	STA3_HUMAN	P40763 homo sapien
2	466	97.7	770	1	STA3_MOUSE	P42227 mus musculus
3	466	97.7	770	1	STA3_RAT	P52631 rattus norv
4	459	96.2	770	1	STA3_BOVIN	P61635 bos taurus
5	451	94.5	771	2	Q6DV79	Q6dv79 gallus gall
6	440.5	92.3	108	2	Q704W6	Q704w6 bos taurus
7	432	90.6	769	2	Q9PVX8	Q9pvx8 xenopus lae
8	427	89.5	766	2	Q7ZXK3	Q7zxk3 oryzias lat
9	381	79.9	765	2	Q6DVF3	Q6dve3 oryzias lat
10	381	79.9	785	2	Q6GUE7	Q6gue7 oryzias lat
11	379	79.5	414	2	Q7ZTS5	Q7zt85 brachydanio
12	379	79.5	786	2	Q6NV46	Q6nv46 brachydanio
13	379	79.5	806	2	Q93599	Q93599 brachydanio
14	375	78.6	767	2	O13133	O13133 oncorhynch
15	374	78.4	764	2	Q90Y16	Q90y16 tetraodon f
16	173	36.3	748	1	STA4_HUMAN	O14765 homo sapien
17	170	35.6	712	2	Q99K94	Q99k94 mus musculus
18	170	35.6	749	1	STA1_MOUSE	P42225 mus musculus
19	170	35.6	749	2	Q8C3V4	Q8c3v4 mus musculus
20	170	35.6	749	2	Q8C497	Q8c497 mus musculus
21	170	35.6	749	2	Q9D323	Q9d323 mus musculus
22	170	35.6	755	2	Q8C9M3	Q8c9m3 mus musculus
23	169	35.4	757	2	Q764M5	Q764m5 sus scrofa
24	168	35.2	712	2	Q6P6Q7	Q6p6q7 rattus norv
25	168	35.2	737	2	Q90Y15	Q90y15 tetraodon f
26	168	35.2	749	2	Q9QXK0	Q9qxk0 rattus norv
27	168	35.2	1165	2	Q7TP57	Q7tp57 rattus norv
28	163	34.2	657	2	Q8AW24	Q8aw24 brachydanio
29	162.5	34.1	718	2	Q801Y2	Q801y2 carassius a
30	161	33.8	748	2	Q66HB2	Q66hb2 rattus norv
31	160.5	33.6	749	1	STA4_MOUSE	P42228 mus musculus

32	158	33.1	750	1	STA1_HUMAN	P42224 homo sapien
33	158	33.1	750	2	Q68D00	Q68d00 homo sapien
34	156	32.7	752	2	Q8JF08	Q8jfg8 brachydanio
35	155	32.5	751	2	Q8JGNO	Q8jgn0 xenopus lae
36	154	32.3	651	2	Q7Z253	Q7zz53 brachydanio
37	154	32.3	667	2	Q8AW20	Q8aw20 brachydanio
38	153.5	32.2	652	2	Q7Z277	Q7zz77 brachydanio
39	153	32.1	553	2	Q8JF07	Q8jfg7 brachydanio
40	147	30.8	754	2	O13131	O13131 oncorhynch
41	146	30.6	749	2	O93598	O93598 brachydanio
42	146	30.6	749	2	Q6P943	Q6p943 brachydanio
43	134	28.1	754	2	O13132	O13132 oncorhynch
44	123	25.8	758	2	Q90Y17	Q90y17 tetraodon f
45	121	25.4	1153	2	Q8JF55	Q8jfg5 brachydanio

ALIGNMENTS

RESULT 1	STA3_HUMAN	STANDARD;	PRT;	770 AA.
ID	STA3_HUMAN	STANDARD;	PRT;	770 AA.
AC	P40763; O14916; Q9BW54;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Signal transducer and activator of transcription 3 (Acute-phase response factor).			
DE	Name=STAT3; Synonyms=APRF;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;			
RA	Yoshida K., Sudo T., Naruto M., Kishimoto T.;			
RT	"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling pathway.";			
RT	Cell 77:63-71(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;			
RA	Della Pietra L., Bresan A., Pezzotti A., Serlupi-Crescenzi O.;			
RT	"Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence.";			
RL	Gene 213:119-124(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.			
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,			
RA	Rajkumar N., Yi Q., Nickerson D.A.;			
RT	"Seatlensf. NBLBI HL66862 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).			
RC	TISSUE=Kidney, and Pancreas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villaion D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN SEQUENCE OF 564-704 FROM N.A.
RN RP
RN TSUVE=Liver;
RN RC
RN Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
RN Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RN PHOSPHORYLATION ON SERINE.
RN RX MEDLINE=95215843; PubMed=7701321;
RN RA Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
RN "Requirement of serine phosphorylation for formation of STAT-promoter
RN complexes";
RN Science 267:1990-1994(1995).
RN [7]
RN INTERACTION WITH NCOAL.
RN RX PubMed=11773079; DOI=10.1074/jbc.M111486200;
RN RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
RN "Functional interaction of STAT3 transcription factor with the
RN coactivator NcoA/SRC1a";
RN J. Biol. Chem. 277:8004-8011(2002).
RN CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
RN (IL-6)-responsive elements identified in the promoters of various
RN acute-phase protein genes.
RN CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
RN CC -1- SUBUNIT: Forms a homodimer or a heterodimer with NCOAL.
RN CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
RN in response to phosphorylation.
RN CC -1- ALTERNATIVE PRODUCTS:
RN CC Event=Alternative splicing; Named isoforms=2;
RN CC Name=1;
RN CC IsoId=P40763-1; Sequence=Displayed;
RN CC Name=Del-701;
RN CC IsoId=P40763-2; Sequence=VSP_010474;
RN CC -1- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
RN muscle, kidney and pancreas.
RN CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
RN LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
RN is important for the formation of stable DNA-binding STAT3
RN homodimers and maximal transcriptional activity.
RN CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
RN CC -1- SIMILARITY: Contains 1 SH2 domain.
RN CC -----
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RN the European Bioinformatics Institute. There are no restrictions on its
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RN entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
RN or send an email to license@isb-sib.ch).
RN CC -----
RN EMBL; L29277; AAA58374.1; -;
RN EMBL; AJ012463; CAA10032.1; -;
RN EMBL; AY572796; AAS66986.1; -;
RN EMBL; BC000627; AAH00627.1; -;
RN EMBL; BC014482; AAH14482.1; -;
RN EMBL; AF029311; AAB84254.1; -;
RN FIR; A54444; A54444.
RN HSP; P42227; IBL1.
RN TRANSFAC; T01493; -;
RN Genew; HGNC:11364; STAT3.
RN H-InvDB; HIX0013840; -;
RN MIM; 102582; -;
RN GO; GO:0005737; Cytoplasm; TAS.
RN GO; GO:0005634; C:nucleus; TAS.
RN GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .); TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; TAS.
DR GO; GO:0000739; P:neurogenesis; TAS.
DR GO; GO:00007165; P:signal transduction; TAS.
DR InterPro; IPR008967; P53 like DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (by similarity).
FT VARSPLIC 701 701 Missing (in isoform Del-701).
FT FTID=VSP_010474.
FT VARIANT 32 32 O -> K (in dbSNP:1803125).
FT FTID=VAR_018683.
FT VARIANT 143 143 M -> I.
FT CONFLICT 288 288 /FTID=VAR_018679.
FT CONFLICT 460 460 Q -> H (in Ref. 1).
FT CONFLICT 548 548 P -> S (in Ref. 1).
FT CONFLICT 561 561 K -> N (in Ref. 1).
FT CONFLICT 667 667 F -> Y (in Ref. 1).
FT CONFLICT 730 730 V -> L (in Ref. 1).
FT CONFLICT 730 730 T -> A (in Ref. 1).
SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
Query Match 97.7%; Score 466; DB 1; Length 770;
Best Local Similarity 97.9%; Pred. No. 2.4e-31;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VQDLEQKMKVVENLQDDDFNFKTLKSGQMDLNGNQSVTQKMQQLTALDQMR 60
DB 155 VQDLEQKMKVVENLQDDDFNFKTLKSGQMDLNGNQSVTQKMQQLTALDQMR 214
QY 61 RSVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
DB 215 RSVSELAGLLSAMEYVQKTLTDEELADWKRQOI 249
RESULT 2
STAJ_MOUSE STANDARD; PRT; 770 AA.
ID STAJ_MOUSE AC P42227;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=Stat3; Synonyms=Aprf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
RN RP AND 632-640.
RN RC STRAIN=BALB/c; TISSUE=Liver;
RN RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RN RA Akira S., Nishio Y., Inoue M., Wang X.-J., Shi W., Matsusaka T.,
RN Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RN "Molecular cloning of APRE, a novel IFN-stimulated gene factor 3 p91-
RN related transcription factor involved in the gp130-mediated signaling
RN pathway";
RN RL Cell 77:63-71(1994).
RN [2]
RN RP SEQUENCE FROM N.A. (ISOFORM STAT3A).

RC TISSUE=Thymus;
RX MEDLINE=94188718; PubMed=8140422;
RA Zhong Z., Wen Z., Darnell J.E. Jr.;
RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
RL response to epidermal growth factor and interleukin-6.";
RN Science 264:95-98(1994).
[3]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Brain;
RX MEDLINE=95014185; PubMed=7523373;
RA Raz R., Durbin J.E., Levy D.E.;
RT "Acute phase response factor and additional members of the interferon-
RL stimulated gene factor 3 family integrate diverse signals from
RN cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
[4]
RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
RX MEDLINE=96016116; PubMed=7568080;
RA Schaefer T.S., Sanders L.K., Nathans D.;
RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
RL form of Stat3.";
RN Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
[5]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=129/SvJ;
RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
RA Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zon L., Oka T.,
RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
RL zebrafish to mouse.";
RN Genomics 71:150-155(2001).
[6]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=C57BL/6J, and NOD/LtJ;
RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
RA Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zon L., Oka T.,
RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
RL zebrafish to mouse.";
RN Genomics 71:150-155(2001).
[7]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Guichard J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalek U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
RP PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.
RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
RA Wen Z., Zhong Z., Darnell J.E. Jr.;
RT "Maximal activation of transcription by Stat1 and Stat3 requires both
RL tyrosine and serine phosphorylation.";
RN Cell 82:241-250(1995).
[9]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;

RA Becker S., Groner B., Mueller C.W.;
RT "Three-dimensional structure of the Stat3beta homodimer bound to
RN DNA.";
RL Nature 394:145-151(1998).
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
(CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes. STAT3B interacts with the N-terminal
CC part of JUN to activate such promoters in a cooperative way.
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Stat3A;
CC IsoId=P42227-1; Sequence=Displayed;
CC Name=Stat3B;
CC IsoId=P42227-2; Sequence=VSP_006287;
CC Name=Del-701;
CC IsoId=P42227-3; Sequence=VSP_010475;
CC -1- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
CC kidney. STAT3B is also detected in the liver, although in a much
CC less abundant manner.
CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L29278; AAA37254.1; -;
CC EMBL; U06922; AAA19452.1; -;
CC EMBL; U08378; AAA56668.1; -;
CC EMBL; U30709; AAC52612.1; -;
CC EMBL; AF246978; AAL59017.1; -;
CC EMBL; AY299489; AAQ75418.1; -;
CC EMBL; AY299490; AAQ75419.1; -;
CC EMBL; BC003806; AAH03806.1; -;
CC FIR; I49508; I49508.1;
CC PDB; 1BGI; X-ray; A=1-722.
CC TRANSFAC; T01574; -;
CC MGD; MGI:103038; Stat3.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0003677; F:DNA binding; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0016563; F:transcriptional activator activity; IDA.
CC GO; GO:0007259; P:JAK-STAT cascade; IDA.
CC GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
CC InterPro; IPR008967; P53_like_DNA_bnd.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001217; STAT.
CC Pfam; PF00017; SH2; 1.
CC Pfam; PF01017; STAT_alpha; 1.
CC Pfam; PF02864; STAT_bind; 1.
CC Pfam; PF02865; STAT_int; 1.
CC PROSITE; P55001; SH2; 1.
KW 3D-structure; Activator; Acute phase; Alternative splicing;
KW Direct protein sequencing; DNA-binding; Nuclear protein;
KW Phosphorylation; SH2 domain; Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine.

Query Match	94.5%	Score 451;	DB 2;	Length 771;
Best Local Similarity	94.7%;	Pred. No. 4.5e-30;		
Matches 90; Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;

[1]
RN SEQUENCE FROM N. A.
RP
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
RA Asashima M., Yokota T.


```

GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045276; AAH45276.1; -.
DR HSSP; P42227; IBLI.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR01217; STAT.
DR Pfam; PF01017; STAT alpha.1.
DR Pfam; PF02864; STAT_bind.1.
DR Pfam; PF02865; STAT_int.1.
DR GO SEQUENCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;
Query Match 79.5%; Score 379; DB 2; Length 414;
Best Local Similarity 77.3%; Pred. No. 3.1e-24;
Matches 75; Conservative 14; Mismatches 6; Indels 2; Gaps 2;
Qy 1 VQDLEQRMKVLENLQDDPFDNYKTLKSQGDV-QDLNGNQ-SVTRQMQOQLTALDQ 58
Db 154 VQDMEQRMKLENLQDDPFDNYKTLKSAGELSQDLNGNSQAAATRKMSQLEQMLSDQ 213
Qy 59 MRRSIVSELAGLLSAMEYVQKLTITDELADWKRPEI 95
Db 214 LRRQIVTEMAGLLSAMDVFQKNLTDELADWKRROQI 250
RESULT 12
Q6NV46 PRELIMINARY; PRT; 786 AA.
ID Q6NV46 AC Q6NV46;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uslan T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068320.1; -;
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; SH2; 1.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 786 AA; 9039 MW; FC7371D0B0E5447E CRC64;
Query Match 79.5%; Score 379; DB 2; Length 786;
Best Local Similarity 77.3%; Pred. No. 6.2e-24;
Matches 75; Conservative 14; Mismatches 6; Indels 2; Gaps 2;
QY 1 VODLEQKVKVENLODDFDNFYKTLKSGQDM-QDLNGNQ-SVTRQKMOQLMQLTALDQ 58
Db 154 VQDMEQKMKLENLQDDFDNFYKTLKSGELSDGLNGNSQAAATRKMSQLEQMLSDQ 213
QY 59 MRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEI 95
Db 214 LRRQIVTEMAGLSAMDFVQKNLTDEELADWKRROQI 250
RESULT 14
O13133 PRELIMINARY; PRT; 767 AA.
ID O13133
AC O13133;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3.
GN Name=rbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
[1]
RP SEQUENCE FROM N.A.
RP Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -;
DR HSSP; P42227; IBGI.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;
Query Match 79.5%; Score 379; DB 2; Length 786;
Best Local Similarity 77.3%; Pred. No. 6.2e-24;
Matches 75; Conservative 14; Mismatches 6; Indels 2; Gaps 2;
QY 1 VODLEQKVKVENLODDFDNFYKTLKSGQDM-QDLNGNQ-SVTRQKMOQLMQLTALDQ 58
Db 154 VQDMEQKMKLENLQDDFDNFYKTLKSGELSDGLNGNSQAAATRKMSQLEQMLSDQ 213
QY 59 MRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEI 95
Db 214 LRRQIVTEMAGLSAMDFVQKNLTDEELADWKRROQI 250
RESULT 13
O93599 PRELIMINARY; PRT; 806 AA.
ID O93599
AC O93599;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uslan T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068320.1; -;
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; SH2; 1.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 786 AA; 9039 MW; FC7371D0B0E5447E CRC64;
Query Match 79.5%; Score 379; DB 2; Length 786;
Best Local Similarity 77.3%; Pred. No. 6.2e-24;
Matches 75; Conservative 14; Mismatches 6; Indels 2; Gaps 2;
QY 1 VODLEQKVKVENLODDFDNFYKTLKSGQDM-QDLNGNQ-SVTRQKMOQLMQLTALDQ 58
Db 154 VQDMEQKMKLENLQDDFDNFYKTLKSGELSDGLNGNSQAAATRKMSQLEQMLSDQ 213
QY 59 MRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEI 95
Db 214 LRRQIVTEMAGLSAMDFVQKNLTDEELADWKRROQI 250
RESULT 13
O93599 PRELIMINARY; PRT; 806 AA.
ID O93599
AC O93599;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RP Oates A.C.;
RL Thesis (1998), University of Melbourne, Australia.
DR EMBL; AJ005693; CAA06677.1; -;
DR HSSP; P42227; IBGI.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;
Query Match 79.5%; Score 379; DB 2; Length 806;
Best Local Similarity 77.3%; Pred. No. 6.4e-24;
Matches 75; Conservative 14; Mismatches 6; Indels 2; Gaps 2;

Search completed: May 25, 2005, 17:43:41
Job time : 44.5283 secs

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GenCore version 5.1.6
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OM protein - protein: search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 68.6634 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-24
Perfect score: 669
Sequence: 1 IACIGPPNICLDRLNWLIT.....LNYQLKIKVICDKDSGDVAA 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	669	100.0	129	4 AAY72856	Aay72856 Mouse Sta
2	669	100.0	185	4 AAY72855	Aay72855 Mouse Sta
3	669	100.0	223	4 AAY72854	Aay72854 Mouse Sta
4	669	100.0	271	4 AAY72841	Aay72841 Mouse Sta
5	669	100.0	720	5 AAE22055	Aae22055 Human Sta
6	669	100.0	769	5 ABB57164	Abb57164 Mouse ibc
7	669	100.0	769	5 AAE22054	Aae22054 Human Sta
8	669	100.0	769	5 AAE22056	Aae22056 Human pro
9	669	100.0	770	2 AAR72082	Aar72082 Mouse Sta
10	669	100.0	770	2 AAR82995	Aar82995 Mouse liv
11	669	100.0	770	2 AAW03176	Aaw03176 Mouse STA
12	669	100.0	770	2 AAY03768	Aay03768 Human STA
13	669	100.0	770	3 AAB12377	Aab12377 N-termina
14	669	100.0	770	5 AAE14652	Aae14652 Murine ST
15	669	100.0	770	5 ABG69497	Abg69497 Human bai
16	669	100.0	770	6 ABU10476	Abu10476 Mouse STA
17	669	100.0	770	8 ADN04365	Adn04365 Antipeori
18	669	100.0	770	8 ADP54789	Adp54789 Human PRO
19	669	100.0	793	3 AAB58442	Aab58442 Lung canc
20	666	99.6	770	7 ADD44738	Add44738 Rat Prote
21	664	99.3	770	2 AAR82993	Aar82993 Human pla
22	664	99.3	770	4 AAB19964	Aab19964 Human sig
23	664	99.3	770	5 AAE15174	Aae15174 Human Sta
24	664	99.3	770	7 ADD44740	Add44740 Human Pro
25	571	85.4	228	4 AAY72861	Aay72861 Mouse Sta

26	571	85.4	229	4 AAY72850	Aay72850 Mouse Sta
27	571	85.4	229	4 AAY72863	Aay72863 Mouse Sta
28	571	85.4	229	4 AAY72862	Aay72862 Mouse Sta
29	571	85.4	252	4 AAY72846	Aay72846 Mouse Sta
30	554	82.8	229	4 AAY72860	Aay72860 Mouse Sta
31	494	73.8	96	4 AAY72857	Aay72857 Mouse Sta
32	493	73.7	213	4 AAY72851	Aay72851 Mouse Sta
33	493	73.7	236	4 AAY72847	Aay72847 Mouse Sta
34	436	65.2	268	2 AAY72844	Aay72844 Mouse Sta
35	436	65.2	582	2 AAW62996	Aaw62996 Human tru
36	436	65.2	582	6 ABU04748	Abu04748 Human exp
37	436	65.2	582	8 ADH57036	Adh57036 Truncated
38	436	65.2	680	6 ABR59713	AbR59713 Human sig
39	436	65.2	712	2 AAR72079	Aar72079 Human STA
40	436	65.2	712	2 AAW03170	Aaw03170 Human STA
41	436	65.2	712	2 AAW62995	Aaw62995 Human STA
42	436	65.2	712	6 ABU04747	Abu04747 Human exp
43	436	65.2	712	6 ABU04735	Abu04735 Human exp
44	436	65.2	712	6 ABU04745	Abu04745 Human exp
45	436	65.2	712	6 ABU04743	Abu04743 Human exp

ALIGNMENTS

RESULT 1
AAY72856
ID AAY72856 standard; protein; 129 AA.
XX
AC AAY72856;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #14 (249-377 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
XX
FH Key
FT Region
FT 94..110
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"
XX
PN WQ200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000MO-US023822.
XX
PR 31-AUG-1999; 99US-00387418.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
PT Identifying an agent for use in modulating the interaction between
transcription factor c-Jun and a Stat3 protein.
XX
PS Claim 65; Page 80-81; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 249-377
amino acids of Stat3 protein. The invention relates to methods for
identifying interacting regions of transcription factors and methods for
identifying agents which modulates the interaction between a
transcription factor such as c-Jun and a Stat protein such as Stat-1 and
Stat-3, useful for modulating gene transcription e.g., cellular
transformation. These identifying agents are used in the treatment of
dysproliferative diseases and also for treating cancer and psoriasis. A

CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 129 AA;

Query Match 100.0%; Score 669; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 4.2e-69;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQOKVSYKGDPIVQHRPMLER 60
 DB 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQOKVSYKGDPIVQHRPMLER 60
 QY 61 IVELFNLMKSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPELNYOLKIKVCI 120
 DB 61 IVELFNLMKSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPELNYOLKIKVCI 120
 QY 121 DKDSGDVAA 129
 DB 121 DKDSGDVAA 129

RESULT 2
 AAY72855
 ID AAY72855 standard; protein; 185 AA.
 AC AAY72855;
 XX
 DT 31-MAY-2001 (first entry)
 DE Mouse Stat3 protein fragment #13 (193-377 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 150..166
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 DR WPI; 2001-226705/23.
 XX
 FT Identifying an agent for use in modulating the interaction between
 FT transcription factor c-Jun and a Stat3 protein.
 XX
 PS Claim 65; Page 80; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 protein fragment containing 193-377
 CC amino acids of Stat3 protein. The invention relates to methods for
 CC identifying interacting regions of transcription factors and methods for
 CC identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX

SQ Sequence 185 AA;

Query Match 100.0%; Score 669; DB 4; Length 185;
 Best Local Similarity 100.0%; Pred. No. 6.8e-69;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQOKVSYKGDPIVQHRPMLER 60
 DB 57 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQOKVSYKGDPIVQHRPMLER 116
 QY 61 IVELFNLMKSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPELNYOLKIKVCI 120
 DB 117 IVELFNLMKSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPELNYOLKIKVCI 176
 QY 121 DKDSGDVAA 129
 DB 177 DKDSGDVAA 185

RESULT 3
 AAY72854
 ID AAY72854 standard; protein; 223 AA.
 XX
 AC AAY72854;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 protein fragment #12 (155-377 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 188..204
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 DR WPI; 2001-226705/23.
 XX
 FT Identifying an agent for use in modulating the interaction between
 FT transcription factor c-Jun and a Stat3 protein.
 XX
 PS Claim 65; Page 79; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 protein fragment containing 155-377
 CC amino acids of Stat3 protein. The invention relates to methods for
 CC identifying interacting regions of transcription factors and methods for
 CC identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 223 AA;

Query Match 100.0%; Score 669; DB 4; Length 223;

Best Local Similarity 100.0%; Pred. No. 8.7e-69; Mismatches 0; Indels 0; Gaps 0;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWNITSLAESQLQTRQIIKKLELOQKVSYGKDPVQHRPMLER 60
DB 95 IACIGPPNICLDRLNWNITSLAESQLQTRQIIKKLELOQKVSYGKDPVQHRPMLER 154

QY 61 IVELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
DB 155 IVELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 214

QY 121 DKDSGDVAA 129
DB 215 DKDSGDVAA 223

RESULT 4
AAV72841
ID AAV72841 standard; protein; 271 AA.
XX AAV72841;
AC AAV72841;
DT 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #2 (107-377 amino acids).
DE Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX Mus musculus.
OS Mus musculus.
XX Key Location/Qualifiers
FH Region 24. .48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
FT Region 236. .252
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX Claim 65; Page 67-68; 86pp; English.
XX The present sequence is mouse Stat3 protein fragment containing 107-377
CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
CC to c-Jun protein in the cell extract. The invention relates to methods
CC for identifying interacting regions of transcription factors and methods
CC for identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX Sequence 271 AA;

Query Match 100.0%; Score 669; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWNITSLAESQLQTRQIIKKLELOQKVSYGKDPVQHRPMLER 60
DB 143 IACIGPPNICLDRLNWNITSLAESQLQTRQIIKKLELOQKVSYGKDPVQHRPMLER 202

QY 61 IVELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
DB 203 IVELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 262

QY 121 DKDSGDVAA 129
DB 263 DKDSGDVAA 271

RESULT 5
AAE22055
ID AAE22055 standard; protein; 720 AA.
XX AAE22055;
AC AAE22055;
DT 25-JUL-2002 (first entry)
XX Human Stat3beta protein.
DE Human; signal transducer and activator of transcription 3; ischaemia;
KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
KW shock; chronic active hepatitis; adult respiratory distress syndrome;
KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
KW polyompositis; rheumatoid arthritis; autoimmune infertility; anaemia;
KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 713. .714
FT /note= "Encoded by ACA CCA TTC"
XX WO200220032-A1.
XX 14-MAR-2002.
XX 10-SEP-2001; 2001WO-US028254.
XX 08-SEP-2000; 2000US-0231212P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX (UYSF-) UNIV SOUTH FLORIDA.
XX Yu H, Pardoll D, Jove R, Dalton W;
XX WPI; 2002-362218/39.
XX N-PSDB; AAD35066.
XX Modulating angiogenesis and an immune response in an individual, for
PT treating a hypoxic or ischemic condition, comprises administering a
PT compound that modulates the activity of a signal transducer and activator
PT of transcription 3.
XX Disclosure; Page 87-89; 94pp; English.
XX The invention relates to a method of modulating angiogenesis and immune
CC response. Method involves administering to an individual a compound that
CC modulate the activity of signal transducer and activator of transcription
CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing

CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC Stat3beta protein
 CC
 CC SQ Sequence 720 AA;

Query Match 100.0%; Score 669; DB 5; Length 720;
 Best Local Similarity 100.0%; Pred. No. 4.2e-68;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IACIGGPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYGKDPVQHRPMLER 60
 DB 249 IACIGGPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYGKDPVQHRPMLER 308
 QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 DB 369 DKDSGDVAA 377

RESULT 6
 ABB57164
 ID ABB57164 standard; protein; 769 AA.

AC ABB57164;
 XX 07-MAR-2002 (first entry)
 DT Mouse ischaemic condition related protein sequence SEQ ID NO:398.
 DE Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX Mus musculus.
 OS WO200188188-A2.
 FN 22-NOV-2001.
 PD 18-MAY-2001; 2001WO-JP004192.
 PF 18-MAY-2000; 2000JP-00145977.
 PR (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 PA Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX WPI; 2002-034733/04.
 DR N-PSDB; ABI99454.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX Claim 2; Page 1084-1087; 2690pp; English.
 PS The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 XX SQ Sequence 769 AA;

Query Match 100.0%; Score 669; DB 5; Length 769;
 Best Local Similarity 100.0%; Pred. No. 4.6e-68;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IACIGGPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYGKDPVQHRPMLER 60
 DB 249 IACIGGPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYGKDPVQHRPMLER 308
 QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 DB 369 DKDSGDVAA 377

RESULT 7
 AAE22054
 ID AAE22054 standard; protein; 769 AA.

AC AAE22054;
 XX 25-JUL-2002 (first entry)
 DT Human Stat3 protein.
 DE Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 OS Homo sapiens.
 FN WO200220032-A1.
 XX 14-MAR-2002.
 PD 10-SEP-2001; 2001WO-US028254.


```

PR 08-SEP-2000; 2000US-0231212P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
PA (UYSF-) UNIV SOUTH FLORIDA.
XX
PI Yu H, Pardoll D, Jove R, Dalton W;
XX
DR WPI; 2002-362218/39.
DR N-PSDB; AAD35065.
XX
PT Modulating angiogenesis and an immune response in an individual, for
PT treating a hypoxic or ischemic condition, comprises administering a
PT compound that modulates the activity of a signal transducer and activator
PT of transcription 3.
XX
PS Disclosure; Page 83-85; 94pp; English.
XX
CC The invention relates to a method of modulating angiogenesis and immune
CC response. Method involves administering to an individual a compound that
CC modulate the activity of signal transducer and activator of transcription
CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
CC hypoxic or ischemic condition or disorder which is the result of stroke,
CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
CC with neovascularisation. Suppressing an immune response is useful for
CC ameliorating a symptom of an autoimmune disease such as systemic lupus
CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
CC dense deposit disease. The method is useful in preventing or treating
CC specific proliferative and oncogenic disease which includes sarcomas and
CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
CC hypoproliferative disorders, physical trauma, lesions and wounds. The
CC method is also used in gene therapy. The present sequence is human Stat3
CC protein
XX
SQ Sequence 769 AA;

Query Match 100.0%; Score 669; DB 5; Length 769;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICDLRLENWITSLAESQLQTRQQLKLEELQOKYSYKGDPTVQHRPMLER 60
Dd |||||
Dd 249 IACIGPPNICDLRLENWITSLAESQLQTRQQLKLEELQOKYSYKGDPTVQHRPMLER 308
QY 61 IVELFNLKMSAFVVERQCPMPHDPRLVIKTVGTQVFTTKVRLLVKFPPELNYQLKIKVCI 120
Dd |||||
Dd 309 IVELFNLKMSAFVVERQCPMPHDPRLVIKTVGTQVFTTKVRLLVKFPPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Dd |||||
Dd 369 DKDSGDVAA 377

RESULT 8
AAE22056
ID AAE22056 standard; protein; 769 AA.
XX
AC AAE22056;
XX
XX 25-JUL-2002 (first entry)
XX

```

```

DE Human protein related to angiogenesis regulation.
XX
KW Human; signal transducer and activator of transcription 3; ischaemia;
KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
KW shock; chronic active hepatitis; adult respiratory distress syndrome;
KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
KW cirrhosis; hypoproliferative disorder; lesion.
XX
OS Homo sapiens.
XX
XX WO200220032-A1.
PN
XX 14-MAR-2002.
PD
XX 10-SEP-2001; 2001WO-US028254.
PF
XX 08-SEP-2000; 2000US-0231212P.
PR
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX (UYSF-) UNIV SOUTH FLORIDA.
XX
PI Yu H, Pardoll D, Jove R, Dalton W;
XX
XX WPI; 2002-362218/39.
DR
XX Modulating angiogenesis and an immune response in an individual, for
XX treating a hypoxic or ischemic condition, comprises administering a
XX compound that modulates the activity of a signal transducer and activator
XX of transcription 3.
XX
PS Disclosure; Page 83-85; 94pp; English.
XX
CC The invention relates to a method of modulating angiogenesis and immune
CC response. Method involves administering to an individual a compound that
CC modulate the activity of signal transducer and activator of transcription
CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
CC hypoxic or ischemic condition or disorder which is the result of stroke,
CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
CC with neovascularisation. Suppressing an immune response is useful for
CC ameliorating a symptom of an autoimmune disease such as systemic lupus
CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
CC dense deposit disease. The method is useful in preventing or treating
CC specific proliferative and oncogenic disease which includes sarcomas and
CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
CC hypoproliferative disorders, physical trauma, lesions and wounds. The
CC method is also used in gene therapy. The present sequence is human
CC protein related to angiogenesis regulation
XX
SQ Sequence 769 AA;

Query Match 100.0%; Score 669; DB 5; Length 769;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 60
 DB 249 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 308
 QY 61 IVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 DB 369 DKDSGDVAA 377
 RESULT 9
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX AC AAR72082;
 XX 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX KW Mouse Stat3 (19sf6).
 DE
 XX KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX OS Mus sp.
 XX W09508629-A1.
 XX 30-MAR-1995.
 XX 26-SEP-1994; 94WO-US010849.
 XX 24-SEP-1993; 93US-00126588.
 XX 24-SEP-1993; 93US-00126595.
 XX 11-MAR-1994; 94US-00212184.
 XX 11-MAR-1994; 94US-00212185.
 XX (UTRQ) UNIV ROCKEFELLER.
 XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 XX Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX Claim 1; Page 107-110; 160pp; English.
 XX A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct FN field.)
 XX SQ Sequence 770 AA;
 Query Match 100.0%; Score 669; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.6e-68;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 60
 DB 249 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 308
 QY 61 IVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 DB 369 DKDSGDVAA 377

DB 249 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 308
 QY 61 IVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 DB 369 DKDSGDVAA 377
 RESULT 10
 AAR82995
 ID AAR82995 standard; protein; 770 AA.
 XX AC AAR82995;
 XX 25-MAR-1996 (first entry)
 DT
 DE Mouse liver acute phase response factor.
 XX KW Mouse; acute phase response factor; transcription factor; interleukin-6;
 KW signal transmission; liver; antibody; antisense; ribozyme;
 KW antinflammatory; antitumor; hypotensive; therapy.
 XX OS Mus musculus.
 XX EP676469-A2.
 XX 11-OCT-1995.
 XX 29-MAR-1995; 95EP-00104670.
 XX 04-APR-1994; 94JP-00065825.
 XX (KISH/) KISHIMOTO T.
 XX Akira S, Kishimoto T;
 WPI; 1995-346089/45.
 DR N-PSDB; AAT05619.
 XX New acute phase response factor - for developing inhibitory agents for
 PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
 PT diseases.
 XX Claim 10; Page 20-22; 31pp; English.
 XX The sequence represents a mouse acute phase response factor (APRF), a
 CC transcription factor related to signal transduction of interleukin-6 (IL-
 CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
 CC library using a polymerase chain reaction product (amplified using
 CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
 CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
 CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
 CC inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
 CC hypertension, etc
 XX SQ Sequence 770 AA;
 Query Match 100.0%; Score 669; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.6e-68;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 60
 DB 249 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 308
 QY 61 IVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129

Db	369	DKDSGDVAA 377		Db	369	DKDSGDVAA 377	
RESULT 11				RESULT 12			
AAW03176				AAW03768			
ID AAW03176 standard; protein; 770 AA.				ID AAY03768 standard; protein; 770 AA.			
XX				XX			
AC AAW03176;				AC AAY03768;			
XX				XX			
DT 24-OCT-1996 (first entry)				DT 11-JUN-1999 (first entry)			
XX				XX			
DE Mouse STAT4.				DE Human STAT3 allelic variant.			
XX				XX			
KW STAT; STAT4; signal transducer and activator of transcription;				KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;			
KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;				KW Intracellular transcription factor; interleukin-6; medicament; variant;			
KW autoimmune disease; antagonist; therapy.				KW pharmaceutical; autoimmune disease; inflammatory; human.			
XX				XX			
OS Mus sp.				OS Homo sapiens.			
XX				XX			
FH Key				FH Key			
FT Domain				FT Domain			
FT 398..508				FT 398..508			
FT /label= DNA binding domain				FT /label= DNA binding domain			
FT /note= "Claim 3, page 110"				FT /note= "Claim 3, page 110"			
XX				XX			
PN WO9620954-A2.				PN 98EP-00102774.			
XX				XX			
PD 11-JUL-1996.				PD 31-MAR-1999.			
XX				XX			
PF 28-DEC-1995;				PF 18-FEB-1998;			
XX				XX			
PR 06-JAN-1995;				PR 16-SEP-1997;			
XX				XX			
PA (UYRQ) UNIV ROCKEFELLER.				PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.			
XX				XX			
PI Darnell JE, Wen Z, Horvath CM, Zhong Z;				PI Serlupi-Crescenzi O, Della Pietra L;			
XX				XX			
DR WPI; 1996-333941/33.				DR WPI; 1999-192664/17.			
XX				DR N-PSDB; AAT31280.			
XX				XX			
PT New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,				PT New human Signal Transducer and Activator of Transcription 3 (STAT3)			
PT preventing or treating cellular dysfunction, e.g. oncogenesis,				PT allelic variant useful for treatment of autoimmune and inflammatory			
PT inflammation, parasitic disease or autoimmunity.				PT disease.			
XX				XX			
PS Disclosure; Page 87-90; 138pp; English.				PS Claim 2; Page 9-13; 32pp; English.			
XX				XX			
CC Mouse signal transducer and activator of transcription (STAT) protein				CC The present sequence represents a predominant allelic variant of human			
CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from				CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an			
CC ligand-activated receptor kinase complexes followed by nuclear				CC intracellular transcription factor which mediates IL-6 signals. The			
CC translocation and DNA binding to activate transcription. Recombinant				CC 'encoding sequence differs from the original published human STAT3 gene			
CC STAT4 can be obt'd. using cDNA clone 19sf6 (AAT31278) obt'd. from				CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3			
CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also				CC DNA molecule can be used for the recombinant expression of the variant.			
CC AAW03167) capable of both receptor recognition and message delivery via				CC STAT3 protein is useful as a medicament or pharmaceutical composition for			
CC DNA binding in a receptor-ligand specific manner. STAT proteins and their				CC treatment of autoimmune or inflammatory diseases			
CC DNA binding domains (see also AAW03165-75) are useful for screening				CC			
CC antagonists used to inhibit STAT-mediated signal transduction and				CC			
CC activation of transcription				CC			
XX				XX			
SQ Sequence 770 AA;				SQ Sequence 770 AA;			
Query Match				Query Match			
Best Local Similarity 100.0%; Score 669; DB 2; Length 770;				Best Local Similarity 100.0%; Score 669; DB 2; Length 770;			
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQSVYKGDPIVQHRPMLER 60				QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQSVYKGDPIVQHRPMLER 60			
DB 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQSVYKGDPIVQHRPMLER 308				DB 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQSVYKGDPIVQHRPMLER 308			
QY 61 IVELFRNLKSAFVVERQCPMPHDPRLVIKTVQFTTKVRLLVKFPPELNLQKIKVCI 120				QY 61 IVELFRNLKSAFVVERQCPMPHDPRLVIKTVQFTTKVRLLVKFPPELNLQKIKVCI 120			
DB 309 IVELFRNLKSAFVVERQCPMPHDPRLVIKTVQFTTKVRLLVKFPPELNLQKIKVCI 368				DB 309 IVELFRNLKSAFVVERQCPMPHDPRLVIKTVQFTTKVRLLVKFPPELNLQKIKVCI 368			
QY 121 DKDSGDVAA 129				QY 121 DKDSGDVAA 129			
XX				XX			

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AC AAB12377;
XX 08-NOV-2000 (first entry)
XX N-terminal domain of murine STAT-3 protein.
DE STAT; signal transducer and activator of transcription; crystal;
KW drug design; murine.
XX Mus sp.
XX Key Location/Qualifiers
FH 4. .9 /label= Alpha helix 1
FT Region
FT 12. .21 /label= Alpha helix 2
FT Region
FT 19. .21 /label= 3(10) helix of alpha helix 2
FT Region
FT 28. .33 /label= Alpha helix 3
FT Region
FT 35. .40 /label= Alpha helix 4
FT Region
FT 43. .47 /label= Alpha helix 5
FT Region
FT 50. .73 /label= Alpha helix 6
FT Region
FT 77. .96 /label= Alpha helix 7
FT Region
FT 99. .119 /label= Alpha helix 8
XX US6087478-A.
XX 11-JUL-2000.
XX 23-JAN-1998; 98US-00012710.
XX 23-JAN-1998; 98US-00012710.
XX (UYRQ ) UNIV ROCKEFELLER.
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX WPI; 2000-505108/45.
XX New crystals of an N-terminal fragment of a signal transducer and
XX activator of transcription that effectively diffracts x-rays, useful for
XX drug screening and development.
XX Disclosure; Fig 1; 42pp; English.
XX The present invention relates to a crystal of an N-terminal fragment of a
XX signal transducer and activator of transcription (STAT) protein. The
XX crystal effectively diffracts x-rays, allowing the determination of the
XX atomic coordinates of the N-terminal domain to a resolution of greater
XX than 5.0 Angstroms. The present sequence is the N-terminal domain of the
XX murine STAT3 protein. The N-terminal domain enables STAT dimers to
XX interact and bind DNA cooperatively, a mechanism important for gene
XX activation. The crystals are useful in drug screening and development by
XX selecting a potential drug by performing rational drug design with the 3-
XX dimensional structure determined for the crystal
XX SQ Sequence 770 AA;
Query Match 100.0%; Score 669; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IACIGGPNICLDLENWITS LAESQIQTRQIIKKLELOQKVS YKGDPIVQHRPMLER 60
DB 249 IACIGGPNICLDLENWITS LAESQIQTRQIIKKLELOQKVS YKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120

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Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377
RESULT 14
AAE14652
ID AAE14652 standard; protein; 770 AA.
XX AAE14652;
XX 16-JUL-2002 (first entry)
XX Murine STAT3 protein.
XX Signal transducer and activator of transcription; STAT3;
XX drug development; drug discovery; crystal; inflammation; allergy; asthma;
XX leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity;
XX viral disease; growth retardation; murine.
XX Mus sp.
XX Key Location/Qualifiers
FH 1. .130 /note= "Conserved N-terminal domain of the STAT family"
FT Domain
FT US6312887-B1.
XX 06-NOV-2001.
XX 24-APR-2000; 2000US-00556273.
XX 23-JAN-1998; 98US-00012710.
XX (UYRQ ) UNIV ROCKEFELLER.
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX WPI; 2002-033337/04.
XX Identifying compounds that bind to signal transducer and activator of
XX transcription proteins, useful for the production of new drugs.
XX Example; Col 47-50; 44pp; English.
XX The invention relates to methods for detecting compounds that bind to
XX signal transducer and activator of transcription (STAT) proteins for the
XX discovery and development of new drug compounds based on the structural
XX properties of the protein crystal. The methods include: identifying a
XX compound that binds to the N-terminal domain of a STAT protein,
XX identifying a compound that enhances or diminishes the binding of the
XX dimeric STAT proteins to each other and/or their nucleic acid binding
XX site; or identifying a compound that enhances or diminishes the ability
XX of STAT protein dimers to induce the expression of a gene operably under
XX the control of a promoter containing at least two adjacent weak binding
XX sites for STAT protein dimers. The methods are used for identifying new
XX drugs. An antagonist of STAT N-terminal dimeric interactions that
XX inhibits the binding of the STAT dimers to adjacent weak binding sites on
XX a promoter of a gene, could be useful as drugs in the treatment of
XX diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other
XX hand, an agonist of N-terminal dimeric interactions between STAT dimers,
XX can be used as drugs in the treatment of diseases e.g. anaemia,
XX neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and
XX growth retardation. The present sequence is murine STAT3 protein
XX SQ Sequence 770 AA;
Query Match 100.0%; Score 669; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy	1	IACIGGPNICLDRLNNWITSLAESQLQTRQOIKKLEELQQKVSYKGDDIVQHRPMLER	60
Dd	249	IACIGGPNICLDRLNNWITSLAESQLQTRQOIKKLEELQQKVSYKGDDIVQHRPMLER	308
Qy	61	IVELFRNLKMSAFVVERQFCMPMHDPDRPLVIKTGVQFTTKVRLLVKFPPELNTQLKIKVCI	120
Dd	309	IVELFRNLKMSAFVVERQFCMPMHDPDRPLVIKTGVQFTTKVRLLVKFPPELNTQLKIKVCI	368
Qy	121	DKDSGDVAAL	129
Dd	369	DKDSGDVAAL	377

RESULT 15

ABG69497
ID ABG69497 standard; protein; 770 AA.

AC ABG69497;

21-OCT-2002 (first entry)

XX Human bait protein STAT3.

XX
KW
Human; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;

KW non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
KW protein-protein interaction map; PIM; anorectic; metabolic disorder.
KW human, yeast two-hybrid assay; adipocyte; fat protein; NIDDM;

KW protein-protein interaction map; PIM; anorectic; metabolic disorder.

OS Homo sapiens.

AA
PN
WO200253726-A2.

11-JUL-2002.

AA 28-DEC-2001; 2001WO-EP015423.
PF

AA 02-JAN-2001; 2001US-0259377P.
PR

AA
PA
(HYBR-) HYBRIGENICS.

PA (HIBK+) HIBRGENICS.
PA (CNRS) CENT NAT RECH SCI.

PI Legrain P, Marullo S, Jockers R;

WPI: 2002-583612/62.

DR N-PSDB; ABS51033.

Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.

PS Claim 1; Page 54; 125pp; English.

The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocytes encoding the for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells by culturing a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The compound isolated by the method is useful for treating and preventing obesity or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 16.141 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-24
Perfect score: 669
Sequence: 1 IACIGPPNICLDRLNWT.....LNYQLKIKVICDKSGDVAA 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	669	100.0	129	3	US-09-387-418A-24
2	669	100.0	185	3	US-09-387-418A-23
3	669	100.0	223	3	US-09-387-418A-22
4	669	100.0	271	3	US-09-387-418A-9
5	669	100.0	770	1	US-08-369-796-12
6	669	100.0	770	1	US-08-416-581B-9
7	669	100.0	770	2	US-08-852-091-12
8	669	100.0	770	2	US-08-820-754-12
9	669	100.0	770	3	US-08-956-652-12
10	669	100.0	770	3	US-08-956-869-12
11	669	100.0	770	3	US-09-012-710-8
12	669	100.0	770	3	US-08-948-547-12
13	669	100.0	770	3	US-09-364-970-3
14	669	100.0	770	3	US-09-364-970-5
15	669	100.0	770	3	US-09-556-273-8
16	669	100.0	770	3	US-08-956-653A-12
17	669	100.0	770	3	US-09-526-542-2
18	669	100.0	770	4	US-08-212-185-12
19	669	100.0	770	4	US-10-117-087-2
20	669	100.0	770	5	PCT-US95-17025-12
21	664	99.3	770	1	US-08-416-581B-1
22	664	99.3	770	1	US-08-416-581B-5
23	664	99.3	770	3	US-09-087-465-6
24	664	99.3	770	4	US-09-972-800A-6
25	664	99.3	771	1	US-08-276-099A-14
26	664	99.3	771	1	US-08-781-890-14
27	571	85.4	229	3	US-09-387-418A-18

28	571	85.4	229	3	US-09-387-418A-28	Sequence 28, Appl
29	571	85.4	229	3	US-09-387-418A-30	Sequence 30, Appl
30	571	85.4	229	3	US-09-387-418A-31	Sequence 31, Appl
31	571	85.4	252	3	US-09-387-418A-14	Sequence 14, Appl
32	554	82.8	229	3	US-09-387-418A-29	Sequence 29, Appl
33	494	73.8	96	3	US-09-387-418A-25	Sequence 25, Appl
34	493	73.7	213	3	US-09-387-418A-19	Sequence 19, Appl
35	493	73.7	236	3	US-09-387-418A-15	Sequence 15, Appl
36	436	65.2	268	3	US-09-387-418A-12	Sequence 12, Appl
37	436	65.2	582	4	US-09-430-806A-3	Sequence 3, Appl
38	436	65.2	712	1	US-08-369-796-6	Sequence 6, Appl
39	436	65.2	712	2	US-08-852-091-6	Sequence 6, Appl
40	436	65.2	712	2	US-08-820-754-6	Sequence 6, Appl
41	436	65.2	712	3	US-08-956-652-6	Sequence 6, Appl
42	436	65.2	712	3	US-08-956-869-6	Sequence 6, Appl
43	436	65.2	712	3	US-08-948-547-6	Sequence 6, Appl
44	436	65.2	712	3	US-08-956-653A-6	Sequence 6, Appl
45	436	65.2	712	4	US-08-212-185-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-387-418A-24
; Sequence 24, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-387-418A-24

Query Match		100.0%;	Score 669;	DB 3;	Length 129;
Best Local Similarity		100.0%;	Pred. No. 5.5e-69;	Mismatches 0;	Indels 0; Gaps 0;
Matches 129;		Conservative 0;			
QY	1	IACIGPPNICLDRLNWTSLAESQLQTRQTKKLEELQKQKVSYGDPVQHRPML	60		
Db	1	IACIGPPNICLDRLNWTSLAESQLQTRQTKKLEELQKQKVSYGDPVQHRPML	60		
QY	61	IVELFRLMKSAFVVERQPCMPHDPRLVITGVQFTTKVRLLVFPPELNYQLKVC	120		
Db	61	IVELFRLMKSAFVVERQPCMPHDPRLVITGVQFTTKVRLLVFPPELNYQLKVC	120		
QY	121	DKDSDGVAA	129		
Db	121	DKDSDGVAA	129		

RESULT 2

US-09-387-418A-23
; Sequence 23, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS

FILE REFERENCE: 600-1-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 185
TYPE: PRT
ORGANISM: Mus musculus
US-09-387-418A-23

Query Match 100.0%; Score 669; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 8.9e-69;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 57 IACIGPPNICLDRLENWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 116
QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQIKKVICI 120
DB 117 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQIKKVICI 176
QY 121 DKDSGDVAA 129
DB 177 DKDSGDVAA 185

RESULT 3

US-09-387-418A-22
Sequence 22, Application US/09387418A
Patent No. 6391572

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui
APPLICANT: Wzesczynska, Melissa H
APPLICANT: Horvath, Curt M
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 223
TYPE: PRT
ORGANISM: Mus musculus
US-09-387-418A-22

Query Match 100.0%; Score 669; DB 3; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 95 IACIGPPNICLDRLENWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 154
QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQIKKVICI 120
DB 155 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQIKKVICI 214
QY 121 DKDSGDVAA 129
DB 215 DKDSGDVAA 223

RESULT 4

US-09-387-418A-9
Sequence 9, Application US/09387418A
Patent No. 6391572

GENERAL INFORMATION:

APPLICANT: Zhang, Xiaokui

APPLICANT: Wzesczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-1-253
CURRENT APPLICATION NUMBER: US/09/387,418A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 271
TYPE: PRT
ORGANISM: Mus musculus
US-09-387-418A-9

Query Match 100.0%; Score 669; DB 3; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.5e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 143 IACIGPPNICLDRLENWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 202
QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQIKKVICI 120
DB 203 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQIKKVICI 262
QY 121 DKDSGDVAA 129
DB 263 DKDSGDVAA 271

RESULT 5

US-08-369-796-12
Sequence 12, Application US/08369796
Patent No. 5716622

GENERAL INFORMATION:

APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid


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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-369-796-12
Query Match 100.0%; Score 669; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 6
US-08-416-581B-9
; Sequence 9, Application US/08416581B
; Patent No. 5719042
; GENERAL INFORMATION:
; APPLICANT: Kishimoto, Tadimitsu
; APPLICANT: Akira, Shizuo
; TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,581B
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-5825/1994
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-37891
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-416-581B-9
Query Match 100.0%; Score 669; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120

US-08-091-12
; Sequence 12, Application US/08852091
; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-852-091-12
Query Match 100.0%; Score 669; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 8

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US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,754
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-754-12

Query Match 100.0%; Score 669; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IACIGGPPNICLDRLNWNITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGGPPNICLDRLNWNITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 308
Qy 61 IVELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 368
Qy 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 9
US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,652
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-652-12

Query Match 100.0%; Score 669; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IACIGGPPNICLDRLNWNITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGGPPNICLDRLNWNITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLER 308
Qy 61 IVELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 10

US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12
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Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPMPHDPRLPVITGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPMPHDPRLPVITGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

RESULT 12

US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118

QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 11

US-09-012-710-8
; Sequence 8, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-012-710-8

Query Match 100.0%; Score 669; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
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Db 309 IVELFRNLKMSAFVVERQPCMPMPHDPRLPVITGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US/07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-547-12

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DB 369 DKDSGDVAA 377

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US-09-364-970-3
; Sequence 3, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-3
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Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-364-970-5
; Sequence 5, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
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RESULT 15
US-09-556-273-8
; Sequence 8, Application US/09556273
; Patent No. 6312887
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: /09/556,273
; APPLICATION NUMBER: US/09/556,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-556-273-8

Query Match 100.0%; Score 669; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

QM protein - protein search, using sw model

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Perfect score: 669
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Post-processing: Minimum Match 0%

Maximum Match 100%

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	669	100.0	185	13 US-10-090-185-23	Sequence 23, Appl
3	669	100.0	223	13 US-10-090-185-22	Sequence 22, Appl
4	669	100.0	271	13 US-10-090-185-9	Sequence 9, Appli
5	669	100.0	720	15 US-10-380-020-4	Sequence 4, Appli
6	669	100.0	769	15 US-10-380-020-2	Sequence 2, Appli
7	669	100.0	769	15 US-10-380-020-5	Sequence 5, Appli
8	669	100.0	770	11 US-09-876-773-12	Sequence 12, Appl
9	669	100.0	770	14 US-10-045-792-8	Sequence 8, Appli
10	669	100.0	770	14 US-10-038-010-56	Sequence 56, Appl
11	669	100.0	770	14 US-10-117-087-2	Sequence 2, Appli
12	669	100.0	770	17 US-10-639-617-12	Sequence 12, Appl
13	669	100.0	793	9 US-09-925-302-780	Sequence 780, App

14	669	100.0	793	10 US-09-925-302-780	Sequence 780, App
15	666	99.6	770	15 US-10-116-275-329	Sequence 329, App
16	664	99.3	770	15 US-10-116-275-349	Sequence 349, App
17	571	85.4	229	13 US-10-090-185-18	Sequence 18, Appl
18	571	85.4	229	13 US-10-090-185-28	Sequence 28, Appl
19	571	85.4	229	13 US-10-090-185-30	Sequence 30, Appl
20	571	85.4	229	13 US-10-090-185-31	Sequence 31, Appl
21	571	85.4	252	13 US-10-090-185-14	Sequence 14, Appl
22	554	82.8	229	13 US-10-090-185-29	Sequence 29, Appl
23	494	73.8	96	13 US-10-090-185-25	Sequence 25, Appl
24	493	73.7	213	13 US-10-090-185-19	Sequence 19, Appl
25	493	73.7	236	13 US-10-090-185-15	Sequence 15, Appl
26	436	65.2	268	13 US-10-090-185-12	Sequence 12, Appl
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29	436	65.2	712	14 US-10-245-120-2	Sequence 2, Appli
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33	436	65.2	750	11 US-09-876-773-4	Sequence 4, Appli
34	436	65.2	750	14 US-10-245-120-1	Sequence 1, Appli
35	436	65.2	750	14 US-10-308-279-44	Sequence 44, Appl
36	436	65.2	750	16 US-10-755-889-352	Sequence 352, App
37	436	65.2	750	16 US-10-755-889-823	Sequence 823, App
38	436	65.2	750	17 US-10-492-043-19	Sequence 19, Appl
39	436	65.2	750	17 US-10-639-617-4	Sequence 4, Appli
40	436	65.2	786	9 US-09-925-297-550	Sequence 550, App
41	432	64.6	749	9 US-09-833-205-4	Sequence 4, Appli
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44	395	59.0	749	14 US-10-045-792-7	Sequence 7, Appli
45	395	59.0	749	14 US-10-205-194-39	Sequence 39, Appli

ALIGNMENTS

RESULT 1
US-10-090-185-24
; Sequence 24, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melisea H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-24

Query Match 100.0%; Score 669; DB 13; Length 129;
Best Local Similarity 100.0%; Pred. No. 9.6e-67;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	IIVELPRLMKSAFVVERQCPMPHDPRLVITKGVQFTTKVRLLVKFPPELNYQLKIKVCI	120
Db	61	IIVELPRLMKSAFVVERQCPMPHDPRLVITKGVQFTTKVRLLVKFPPELNYQLKIKVCI	120

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; Sequence 23, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
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; ORGANISM: Mus musculus
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US-10-090-185-23

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; Sequence 22, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
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US-10-090-185-22

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; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
;
US-10-090-185-9

Query Match      100.0%; Score 669; DB 13; Length 271;
Best Local Similarity 100.0%; Pred. No. 2.5e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IACIGPPNICLDRLNWTSLAESQLQTRQIQKLEELQKVSXKGDPIVQHRPMLER 60
      |||||
Db      143 IACIGPPNICLDRLNWTSLAESQLQTRQIQKLEELQKVSXKGDPIVQHRPMLER 202

QY      61 IVELFRLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
      |||||
Db      203 IVELFRLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 262

QY      121 DKDSGDVAA 129
      |||||
Db      263 DKDSGDVAA 271

RESULT 5
US-10-380-020-4
; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 4
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; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match      100.0%; Score 669; DB 15; Length 720;
Best Local Similarity 100.0%; Pred. No. 8.8e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 6
US-10-380-020-2
; Sequence 2, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT<
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match      100.0%; Score 669; DB 15; Length 769;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 7
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
```

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; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match      100.0%; Score 669; DB 15; Length 769;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 8
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Fu, Xian-Yuan
; Schindler, Christian W.
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 100.0%; Score 669; DB 11; Length 770;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308
QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
Db 309 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 9

US-10-045-792-8
Sequence 8, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe

Moarefi, Iemal
Darnell, Jr., James E.
Kurlyan, John

TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPL APPLICATION NUMBER: US/10/045,792

FILING DATE: 19-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPL APPLICATION NUMBER: US/09/012,710

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-194

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 770 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8

Query Match 100.0%; Score 669; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308
QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
Db 309 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 10

US-10-038-010-56

Sequence 56, Application US/10038010

Publication No. US20030040089A1

GENERAL INFORMATION:

APPLICANT: HYBRIGENICS

APPLICANT: Pierre, Legrain

TITLE OF INVENTION: Protein-protein interactions in adipocyte cells

FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

PRIOR FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/259,377

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patent in version 3.1

SEQ ID NO 56

LENGTH: 770

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: STAT3 : Transcription factor

LOCATION: (1)-(770)

OTHER INFORMATION:

US-10-038-010-56

Query Match 100.0%; Score 669; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308
QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
Db 309 IVELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 11

US-10-117-087-2

Sequence 2, Application US/10117087

Publication No. US20030166854A1

GENERAL INFORMATION:

APPLICANT: SERLUPI-CRESCENZI, Ottaviano

APPLICANT: DELLA PIETRA, Linda

;; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
;; FILE REFERENCE: SERLUPI-2
;; CURRENT APPLICATION NUMBER: US/10/117,087
;; CURRENT FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US/09/526,542
;; PRIOR FILING DATE: 2000-03-19
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patent in version 3.0
;; SEQ ID NO 2
;; LENGTH: 770
;; TYPE: PRT
;; ORGANISM: Human
US-10-117-087-2

Query Match 100.0%; Score 669; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 60
Db 249 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 308

Qy 61 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 368

Qy 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 12

US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/639,617
; FILING DATE: 12-Aug-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 100.0%; Score 669; DB 17; Length 770;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 60
Db 249 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 308

Qy 61 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 368

Qy 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 13

US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match 100.0%; Score 669; DB 9; Length 793;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 60
Db 272 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 331

Qy 61 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
Db 332 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 391

Qy 121 DKDSGDVAA 129
Db 392 DKDSGDVAA 400

RESULT 14

US-09-925-302-780

R; Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.;

Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRE, a novel IFN-stimulated gene factor 3 p91-related transmembrane protein
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in eukaryotic cells
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
C;Genetics:
A;Gene: GDB:STAT3; APRE
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor

Query Match 99.3%; Score 664; DB 2; Length 770;
Best Local Similarity 99.2%; Pred. No. 5.5e-55;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRLNWTSLAESQLOTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLNWTSLAESQLOTRQIKKLEELHOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPELNYQIKKVC 120
DB 309 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPELNYQIKKVC 368
QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91- and 84-kDa ISGF-3 subunits
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 58.4%; Score 390.5; DB 2; Length 739;
Best Local Similarity 60.7%; Pred. No. 4.3e-29;
Matches 74; Conservative 18; Mismatches 19; Indels 11; Gaps 1;
QY 2 ACIGPPNICLDRLNWTSLAESQLOTRQIKKLEELQOKVSYKGDPIVQHRPMLERI 61
DB 246 ACIGPPNACLDLQ-----QVRQOKKLEELQKYTYEHPITKKNQVLWRT 294
QY 62 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPELNYQIKKVCID 121
DB 295 FSLFQQLIQSSFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKQLQELNYNLKVKVLF 354
QY 122 KD 123
DB 355 KD 356

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, M.L. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in eukaryotic cells
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:g509502; PID:AAA19692.1; PID:g50950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 56.1%; Score 375; DB 2; Length 748;
Best Local Similarity 59.3%; Pred. No. 1.3e-27;
Matches 73; Conservative 19; Mismatches 31; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRLNWTSLAESQLOTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 244 IACIGPPNGLDQLQCNCFLLAESLFQRLQOKLEQSTKMTYEGDPIPAQRAHLLER 303
QY 61 IVELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPELNYQIKKVC 120
DB 304 ATELLYNLFKNSFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPELNYQIKKVC 363
QY 121 DKD 123
DB 364 DKN 366

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
N;Alternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-851 <FU>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
submitted to the EMBL Data Library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:g1293919; PID:AAA98760.1; PID:g1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in the human genome
A;Reference number: S53873; MUID:95192056; PMID:7885841
A;Accession: S53873
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-196;392-591;684-730 <YAN>
A;Cross-references: EMBL:U18671
C;Genetics:
A;Gene: stat2
A;Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 411/2
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: signal transduction; transcription regulation

Query Match 38.4%; Score 257; DB 2; Length 851;
Best Local Similarity 42.6%; Pred. No. 2.3e-16;
Matches 52; Conservative 25; Mismatches 45; Indels 0; Gaps 0;

A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A;Residues: 1-793 <MUI>
A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIA0; EMBL:Z48538; NID:g758633; PIDN:CANA
R:Liu, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologous (Stat5b) involved
in cytokine signaling
A;Reference number: I49273; MUID:96004632; PMID:7568026
A;Accession: I49273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-793 <RES>
A;Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972
C;Genetics:
A;Gene: Stat5a
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 24.0%; Score 160.5; DB 2; Length 793;
Best Local Similarity 37.6%; Pred. No. 3e+07;
Matches 38; Conservative 17; Mismatches 37; Indels 9; Gaps 2;

Qy 5 GGPNICLDRLNWITS LAESQLTROQIKLEELQKVSKGDPVQHPRMLERIVEL 64
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 265 GGPPEGSLDLQSCEKLAETIWNQQIRAEHLCOQLPIPG-EVEEMLAEVNATITDI 323
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 65 FRNLKSAFVVVERPCMPHMDPLVIKTGVQFTTKVRLLV 105
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 324 ISALVTSTFIEIKQP-----PQVLTKQTQFAATVRLLV 356
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 8
G02317
transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
R;Lin, J.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g1151169
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 24.0%; Score 160.5; DB 2; Length 794;
Best Local Similarity 37.6%; Pred. No. 3e+07;
Matches 38; Conservative 17; Mismatches 37; Indels 9; Gaps 2;

Qy 5 GGPNICLDRLNWITS LAESQLTROQIKLEELQKVSKGDPVQHPRMLERIVEL 64
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 265 GGPPEGSLDLQSCEKLAETIWNQQIRAEHLCOQLPIPG-EVEEMLAEVNATITDI 323
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 65 FRNLKSAFVVVERPCMPHMDPLVIKTGVQFTTKVRLLV 105
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 324 ISALVTSTFIEIKQP-----PQVLTKQTQFAATVRLLV 356
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 9
S55527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Guilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regulato
ry family
A;Reference number: S55527; MUID:95188889; PMID:7882987
A;Accession: S55527
A:Molecule type: mRNA

C;Genetics:
A;Gene: STAT6
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 14.0%; Score 93.5; DB 2; Length 837;
Best Local Similarity 32.4%; Pred. No. 0.71;
Matches 33; Conservative 12; Mismatches 38; Indels 19; Gaps 3

QY 5 GGPNNICLDLENWITSLAESQLOTRQIIKKLE-ELQOKVSYKGDPIVQHRPMLERIVE 63
DB 214 GTFPESLAGQRCESLVSIYQHQEIGAASGELEPKT-----RASLISRLDE 263
QY 64 LFNLMKSAFWERQPCMPHDPRLPVIKTGVQFTTKVRLIV 105
DB 264 VLRLTVSSFLVEKQP-----PQVLKTQTKFQAGVRFL 297

RESULT 12
H90279
microtubule binding protein, probable [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90279
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.;
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.;
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <KUR>
A;Cross-references: UNIPROT:Q9UXN4; GB:A5006641; NID:gl3814451; PIDN:AAK41495.1
C;Genetics:
A;Gene: SSO1256

Query Match 12.0%; Score 80.5; DB 2; Length 464;
Best Local Similarity 27.9%; Pred. No. 6;
Matches 39; Conservative 25; Mismatches 41; Indels 35; Gaps 7

QY 14 RLENWITSLAESQLOTRQIIKKLEELQOKV--SYKG--DPVQHRPML-----E 58
DB 280 KLENAVEQLVEAQRDTRITKLEEVTKMLVESQLGMQNEIRELRKALGSMGKRWGRDPE 339
QY 59 ERIVELFRNLMK-----SAFVVRQPCMPHDPRLPVIKTGVQFTTKVRLIVKFPPE 109
DB 340 KLIIIEVDELAQEGDLKYYNKETYK-----DDNGLFGLKGVEY--DVDLLIKDTK 389

QY 110 LNTYOLTKVICIDKDSGDVAA 129
DB 390 V-VLIEIKSYVEKDDVNWAA 408

RESULT 13
T21C12
hypothetical protein T21C12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C;Accession: T21C12
R;Wilkinson, J.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19976
A;Accession: T21C12
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-393 <WIL>
A;Cross-references: UNIPROT:Q22633; EMBL:Z50016; PIDN:CAA90315.1; GSPDB:GN0002
A;Experimental source: clone T21C12
C;Genetics:
A;Gene: CESP:T21C12.2
A;Map position: 3
A;Introns: 137/3; 236/3

C;Superfamily: 4-hydroxyphenylpyruvate_dioxygenase

Query Match 12.0%; Score 80; DB 2; Length 393;
Best Local Similarity 20.8%; Pred. No. 5.5;
Matches 35; Conservative 23; Mismatches 56; Indels 54; Gaps 6;

QY 3 CIGPPNICLDRLNW-----ITSLAESQLQTRQI----- 33
DB 183 CVGNQPLQMSAVOMTEKVKLHFRFWSVDDSMIHTBSALRSIVTNFETIMPNP 242
QY 34 -----KKLEELQKVSQKGPPIVQHRPMLERIVEL-----FRNLKMGAF--VVE 76
DB 243 ATSDKKAISQIQEVDYGGSGVQHIALNTSDIITAEALRARCCEFLSPSSVDYDLKE 302
QY 77 RQCPMPHPRPLVIKTVGFTTKVRLLVKPELNYOLKI--KVICDK 122
DB 303 RLAASSM-----VVKEDMDRLQKLHILVDFDENGYLLOIFSKPQQR 344

RESULT 14

NDECAS

type I site-specific deoxyribonuclease (RC 3.1.21.3) EcoA chain S - Escherichia coli
N;Alternate names: deoxyribonuclease, EcoA, S chain (ATP- and S-adenosyl-L-methionine-de
C;Species: Escherichia coli
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 30-Jun-1993
C;Accession: A32343
R;Cowan, G.M.; Gann, A.A.F.; Murray, N.E.
Cell 56, 103-109, 1989
A;Title: Conservation of complex DNA recognition domains between families of restriction
A;Reference number: A32343; MUID:89089749; PMID:2642743

A;Accession: A32343

A;Molecule type: DNA

A;Residues: 1-589 <COW>

C;Comment: This S chain, one of three components (S, R, and M chains) of type I, site-spe

confer specificity for the target sequence, GAG.

C;Superfamily: type I site-specific deoxyribonuclease EcoA chain S

C;Keywords: DNA binding; hydrolase; restriction modification system

Query Match 11.8%; Score 79; DB 1; Length 589;
Best Local Similarity 24.4%; Pred. No. 11;
Matches 31; Conservative 25; Mismatches 41; Indels 30; Gaps 6;

QY 10 ICDRLNWTSLAESQLQTRQ-----IKLEELQKVSQK-----DPV 51
DB 6 LIVDHMETW-----TSALQTRTAGRSSGKIDLYGIKKRLLELAVRGKLVPDPND 60

QY 52 QHRPMLERIVELFRNLKSAFVVERQPCMP--MHPDRPLVIKTVGFTTKVRLLVKPE 109
DB 61 EPASLLKRIAEBKAELVKQGIKKQKP-LPEISBEKPELPDGEWTT----LRIAE 115

QY 110 LNYOLKI 116

DB 116 INPKIDV 122

RESULT 15

B70042

hypothetical protein yviE - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: B70042

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B70042
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <KUN>
A;Cross-references: UNIPROT:P96502; GB:299122; GB:AL009126; NID:g2636029; PIDN:CAB15555
A;Experimental source: strain 168
C;Genetics:
A;Gene: yviE
C;Superfamily: Bacillus subtilis hypothetical protein yviE

Query Match 11.7%; Score 78.5; DB 2; Length 191;
Best Local Similarity 20.9%; Pred. No. 3.3;
Matches 31; Conservative 25; Mismatches 41; Indels 51; Gaps 7;

QY 7 PPNICLDRLNWTSLAESQLQTRQIKLEELQ-----KVS 45
DB 48 PGKLTIDQTOAW-----EELDRKHVFKRIEAAQOQHEDVMEGIARTABEGDELMKIE 101
QY 46 KGPPIV-QHRPMLERIVELFRNLKMS-----AFVVERQPCMPHPRPLV 90
DB 102 KGNPIASQARRNSEMHIQIGENYAFSLSRVKIQYTPSQLDVQITPRKPVQAEPRPI- 160
QY 91 IKTVGQFT---TKVRLLVKPELNYOLK 115
DB 161 ----VEYTPGNVVDML-QYPDLNIDVE 183

Search completed: May 25, 2005, 17:45:25

Job time : 14.1698 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 53.6753 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-24

Perfect score: 669

Sequence: 1 IACIGPPNICLDRLNWT.....LNYQLKIKCIDKSGDVAA 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	669	100.0	163	Q9N145	Q9N145 macaca mula
2	669	100.0	770	1 STA3 BOVIN	P61635 bos taurus
3	669	100.0	770	1 STA3 HUMAN	P40763 homo sapien
4	669	100.0	770	1 STA3 MOUSE	P42227 mus musculus
5	666	99.6	770	1 STA3 RAT	P52631 rattus norv
6	665	99.4	771	2 Q6DV79	Q6dv79 gallus gall
7	658	98.4	769	2 Q9PVX8	Q9pvx8 xenopus lae
8	650	97.2	766	2 Q7ZXX3	Q7zxx3 xenopus lae
9	637	95.2	786	2 Q6NV46	Q6nv46 brachydanio
10	637	95.2	806	2 Q93599	Q93599 brachydanio
11	635	94.9	785	2 Q6DVF3	Q6dvf3 oryzias lat
12	635	94.9	785	2 Q6GUE7	Q6gue7 oryzias lat
13	635	94.9	785	2 Q90Y16	Q90y16 tetraodon f
14	624	93.3	764	2 Q13133	O13133 oncorhynch
15	600	89.7	767	2 Q13133	O13133 oncorhynch
16	555	83.0	161	2 Q704W5	Q704w5 bos taurus
17	446	66.7	751	2 Q8JGN0	Q8jgn0 xenopus lae
18	436	65.2	750	1 STA3 HUMAN	P42224 homo sapien
19	436	65.2	750	2 Q68D00	Q68d00 homo sapien
20	434	64.9	758	2 Q90Y17	Q90y17 tetraodon f
21	432	64.6	712	2 Q6P6Q7	Q6p6q7 rattus norv
22	432	64.6	749	2 Q90XK0	Q90xk0 rattus norv
23	430	64.3	757	2 Q764M5	Q764m5 sus scrofa
24	428	64.0	749	2 Q8C497	Q8c497 mus musculus
25	427	63.8	712	2 Q99K94	Q99k94 mus musculus
26	427	63.8	749	2 Q8C3V4	Q8c3v4 mus musculus
27	427	63.8	749	2 Q9D323	Q9d323 mus musculus
28	427	63.8	755	2 Q8C8M3	Q8c8m3 mus musculus
29	422	63.1	754	2 O13131	O13131 oncorhynch
30	415	62.0	1153	2 Q8JFS5	Q8jfs5 brachydanio
31	410	61.3	754	2 O13132	O13132 oncorhynch

32 409 61.1 528 2 Q8JFU8
33 406 60.7 718 2 Q801Y2
34 395 59.0 749 1 STA1 MOUSE
35 386 57.7 749 2 Q93598
36 386 57.7 749 2 Q6P943
37 379 56.7 748 1 STA4 HUMAN
38 375 56.1 749 1 STA4 MOUSE
39 374 55.9 748 2 Q66HB2
40 373 55.8 553 2 Q8JFU7
41 373 55.8 651 2 Q7Z253
42 373 55.8 652 2 Q7Z277
43 373 55.8 657 2 Q8AW24
44 373 55.8 667 2 Q8AW20
45 359 53.7 737 2 Q90Y15

Q8jfu8 brachydanio
Q801y2 carassius a
P42225 mus musculu
Q93598 brachydanio
Q6p943 brachydanio
Q14755 homo sapien
P42228 mus musculu
Q66hb2 rattus norv
Q8jfu7 brachydanio
Q7z253 brachydanio
Q7z277 brachydanio
Q8aw24 brachydanio
Q8aw20 brachydanio
Q90y15 tetraodon f

ALIGNMENTS

RESULT 1

Q9N145 PRELIMINARY; PRT; 163 AA.
ID Q9N145
AC Q9N145;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Name=STAT3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227560; AAF73401.1; -;
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR NON_TER 1
FT NON_TER 163 163
SQ SEQUENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;

Query Match 100.0%; Score 669; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 7.6e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESLQTRQIQKLEELQOKVSYKGDPIVQHRPMLER 60
|||||
19 IACIGPPNICLDRLNWTSLAESLQTRQIQKLEELQOKVSYKGDPIVQHRPMLER 78
|||||
QY 61 IVELFNLMLKSAFVVERQCPMPHDPRLPIVKTGVTTKVRLLVKFPPELNYQLKIKVCI 120
|||||
79 IVELFNLMLKSAFVVERQCPMPHDPRLPIVKTGVTTKVRLLVKFPPELNYQLKIKVCI 138
|||||

QY 121 DKDSGDVAA 129
|||||

DB 139 DKDSGDVAA 147
|||||

RESULT 2

STA3_BOVIN STANDARD; PRT; 770 AA.
ID STA3_BOVIN
AC P61635;

05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=STAT3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCB1_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RT "The STAT3B-encoding gene was flipped across the STAT3/STAT5A-locus
RL during ruminant evolution."; EMBL/GenBank/DBJ databases.
CC Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes (By similarity).
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ620655; CAF06182.1; -
DR PROSITE; PS50001; SH2; 1.
KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73EB3274 CRC64;

Query Match 100.0%; Score 669; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-54;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IACIGGPPNICLDRLENWITSLAESQLQTRQIKLEELQKVSYGKDPVQHRPMLER 60
Db 249 IACIGGPPNICLDRLENWITSLAESQLQTRQIKLEELQKVSYGKDPVQHRPMLER 308

Qy 61 IVELFRNLMSAFVVERQPCMPHDPRLVIKGTQVFTKRLLVKPELNLQIKKVC 120
Db 309 IVELFRNLMSAFVVERQPCMPHDPRLVIKGTQVFTKRLLVKPELNLQIKKVC 368

Qy 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 3
STA3 HUMAN STANDARD; PRT; 770 AA.
AC P40763; O14916; Q9EW54;
DT 01-FEB-1995 (Rel. 31, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
DE Name=STAT3; Synonyms=APRF;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RA Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRF, a novel IFN- γ -stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway."; Cell 77:63-71 (1994).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
RT "Highly conserved amino-acid sequence between murine STAT3 and a
RT revised human STAT3 sequence."; Gene 213:119-124 (1998).
RL [3]
RP SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattlesNP. NHLBI HL66682 program for genomic applications, UW-
RT PHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
RC TISSUE=Kidney, and Pancreas;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [5]
RP SEQUENCE OF 564-704 FROM N.A.
RC TISSUE=Liver;
RA Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP PHOSPHORYLATION ON SERINE.
RC MEDLINE=95215843; PubMed=7701321;
RA Zhang X., Blienis J., Li H.-C., Schindler C., Chen-Kiang S.;
RT "Requirement of serine phosphorylation for formation of STAT-promoter
RT complexes."; Science 267:1990-1994 (1995).
RL [7]
RP INTERACTION WITH NCOAL.
RC PubMed=11773079; DOI=10.1074/jbc.M111486200;
RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
RT "Functional interaction of STAT3 transcription factor with the
RT coactivator NCOA/SRC1a."; J. Biol. Chem. 277:8004-8011 (2002).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.

CC -!- PATHWAY: Involved in the gpi30-mediated signaling pathway.
 CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P40763-1; Sequence=Displayed;
 CC Name=Del-701;
 CC IsoId=P40763-2; Sequence=VSP_010474;
 CC TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
 CC muscle, kidney and pancreas
 CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity.
 CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -----
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 CC -----
 CC EMBL; L29277; AA58374.1; -;
 CC EMBL; AJ012463; CAAL0032.1; -;
 CC EMBL; AY572796; AAS66986.1; -;
 CC EMBL; BC000627; AAH00627.1; -;
 CC EMBL; BC014482; AAH14482.1; -;
 CC EMBL; AF029311; AAB84254.1; -;
 CC PIR; A54444; A54444.
 CC HSP; P42227; LBGI.
 CC TRANSFAC; T01493; -;
 CC Genew; HGNC:11364; STAT3.
 CC H-invDB; HIX0013840; -;
 CC MIM; 102582; -;
 CC GO; GO:0005737; Cytoplasm; TAS.
 CC GO; GO:0005634; Cnucleus; TAS.
 CC GO; GO:0003062; Farnesoyltransferase/interferon-class (D200-domain...); TAS.
 CC GO; GO:0003700; Farnesoyltransferase/interferon-class (D200-domain...); TAS.
 CC GO; GO:0006928; P:cell motility; TAS.
 CC GO; GO:0007259; P:JAK-STAT cascade; TAS.
 CC GO; GO:0001222; P:negative regulation of transcription from P...; TAS.
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR008967; P53_like_DNA_bnd.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001217; STAT.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF01017; STAT_alpha; 1.
 CC Pfam; PF02864; STAT_bind; 1.
 CC Pfam; PF02865; STAT_int; 1.
 CC PROSITE; PS00011; SH2; 1.
 CC Activator; Alternative splicing; DNA-binding; Nuclear protein;
 CC Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
 CC DOMAIN 580 670 SH2.
 CC MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 CC MOD_RES 727 727 Phosphoserine (By similarity).
 CC VARSPLIC 701 Missing (in isoform Del-701).
 CC /FTId=VSP_010474.
 CC Q -> K (in dbSNP:1803125).
 CC /FTId=VAR_018683.
 CC VARIANT 32 32 M -> I.
 CC VARIANT 143 143 /FTId=VAR_018679.
 CC CONFLICT 288 288 Q -> H (in Ref. 1).
 CC CONFLICT 460 460 P -> S (in Ref. 1).
 CC CONFLICT 548 548 K -> N (in Ref. 1).
 CC CONFLICT 561 561 F -> Y (in Ref. 1).
 CC CONFLICT 667 667 V -> L (in Ref. 1).

FT CONFLICT 730 730 T -> A (in Ref. 1).
 SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
 Query Match 100.0%; Score 669; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.6e-54;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IACIGPPNICLDRLNENWITSLAESOLQTRQIKLEELQKKVSYKGDPTVQHRPMLER 60
 |||||||
 DB 249 IACIGPPNICLDRLNENWITSLAESOLQTRQIKLEELQKKVSYKGDPTVQHRPMLER 308
 |||||||
 QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVKTGVOFTTKVRLVLKPELNYQLKVKCI 120
 |||||||
 DB 309 IVELFRLMKSAFVVERQPCMPHDPRLVKTGVOFTTKVRLVLKPELNYQLKVKCI 368
 |||||||
 QY 121 DKDSGDVAA 129
 |||||||
 DB 369 DKDSGDVAA 377
 |||||||
 RESULT 4
 STA3 MOUSE
 ID STA3 MOUSE STANDARD; PRT; 770 AA.
 AC P42227;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 GN Name=Stat3; Synonyms=Aprf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
 RP AND 632-640.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
 RA Akira S., Nishio Y., Inoue M., Wang X.-J., Shi W., Matsusaka T.,
 RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
 RT related transcription factor involved in the gp130-mediated signaling
 RT pathway.";
 RL Cell 77:63-71 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC TISSUE=Thymus;
 RX MEDLINE=94188718; PubMed=8140422;
 RA Zhong Z., Wen Z., Darnell J.E. Jr.;
 RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
 RT response to epidermal growth factor and interleukin-6.";
 RL Science 264:95-98 (1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC TISSUE=Brain;
 RX MEDLINE=95014185; PubMed=7523373;
 RA Raz R., Durbin J.E., Levy D.E.;
 RT "Acute phase response factor and additional members of the interferon-
 RT stimulated gene factor 3 family integrate diverse signals from
 RT cytokines, interferons, and growth factors.";
 RL J. Biol. Chem. 269:24391-24395 (1994).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
 RC STRAIN=BALB/c. and C57BL/6; TISSUE=Liver;
 RX MEDLINE=96016116; PubMed=7568080;
 RA Schaefer T.S., Sanders L.K., Nathans D.;
 RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
 RT form of Stat3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101 (1995).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=129/SVJ;


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FT STRAND 338 340
FT TURN 341 342
FT STRAND 345 351

Query Match 100.0%; Score 669; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-54;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 5
STA3 RAT STANDARD; PRT; 770 AA.
AC P52631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=Stat3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liver;
RX MEDLINES=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
RA Ripberger J.A., Fritz S., Richter K., Hocke G.M., Lottgepeich F.,
RA Fey G.H.;
RT "Transcription factors Stat3 and Stat5b are present in rat liver
RT nuclei late in an acute phase response and bind interleukin-6 response
RT elements.";
RL J. Biol. Chem. 270:29998-30006(1995).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.
CC -!- SUBUNIT: Involved in the gp130-mediated signaling pathway.
CC -!- PATHWAY: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOA1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation (By similarity).
CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X91810; CAAG2920.1; -
CC DR HSSP; P42227; 1BG1.
CC DR RGD; 3772; Stat3.
CC DR InterPro; IPR008967; P53_like_DNA_bnd.
CC DR InterPro; IPR000980; SH2.
CC DR InterPro; IPR001217; STAT.

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DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 88039 MW; D74AOC76954754ED CRC64;

Query Match 99.6%; Score 666; DB 1; Length 770;
Best Local Similarity 99.2%; Pred. No. 8.7e-54;
Matches 128; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 6
Q6DV79 PRELIMINARY; PRT; 771 AA.
ID Q6DV79;
AC Q6DV79;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Signal transducer and activator of transcription 3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF641397; AAF64887.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0003700; F:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match 99.4%; Score 665; DB 2; Length 771;
Best Local Similarity 99.2%; Pred. No. 1.1e-53;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 120

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Db 309 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 Db 369 DKDSGDVAA 377

RESULT 7

Q9PVX8 PRELIMINARY; PRT; 769 AA.
 AC Q9PVX8;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Stat 3.
 GN Name-stat 3;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 CX NCB1_TaxID=8355;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
 RX Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
 RA Aashima M., Yokota T.;
 RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
 RT embryos independent of BMP-4.";
 RL Dev. Biol. 216:481-490(1999).
 DR EMBL; AB017701; BAA86061.1; -.
 DR HSP; P42227; IBG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF000017; SH2; 1.
 DR Pfam; PF01017; STAT alpha; 1.
 DR Pfam; PF02864; STAT bind; 1.
 DR Pfam; PF02865; STAT int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;

Query Match 98.4%; Score 658; DB 2; Length 769;
 Best Local Similarity 98.4%; Pred. No. 4.9e-53;
 Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IACIGGPNICLDLENWITSLAESQLQTRQIKKLELOQKYSYKGDPIVQHRPMLER 60
 Db 249 IACIGGPNICLDLENWITSLAESQLQTRQIKKLELOQKYSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 120
 Db 309 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129

Db 369 DKDSGDVAA 377

RESULT 8

Q7ZXK3 PRELIMINARY; PRT; 766 AA.
 AC Q7ZXK3;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Stat3-A protein.
 GN Name=stat3-A;

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 CX NCB1_TaxID=8355;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RC Klein S., Strausberg R.;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC04717; AAH44717.1; -.
 DR HSP; P42227; IBG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF000017; SH2; 1.
 DR Pfam; PF01017; STAT alpha; 1.
 DR Pfam; PF02864; STAT bind; 1.
 DR Pfam; PF02865; STAT int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;

Query Match 97.2%; Score 650; DB 2; Length 766;
 Best Local Similarity 96.9%; Pred. No. 2.7e-52;
 Matches 125; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IACIGGPNICLDLENWITSLAESQLQTRQIKKLELOQKYSYKGDPIVQHRPMLER 60
 Db 249 IACIGGPNICLDLENWITSLAESQLQTRQIKKLELOQKYSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 120
 Db 309 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 368

Db 250 IACIGPPNICLDRELTWITSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 309
QY 61 IVELFRNLKMSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 120
Db 310 IVDLFRNLKMSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

RESULT 11
Q6DVF3
ID O93599 PRELIMINARY; PRT; 806 AA.
AC O93599
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oates A.C.;
RL Thesis (1998), University of Melbourne, Australia.
DR EMBL; AJ005693; CAA06677.1; -.
DR HSP; P42227; 18G1.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match 95.28; Score 637; DB 2; Length 806;
Best Local Similarity 93.8%; Pred. No. 4.8e-51;
Matches 121; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRELTWITSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 60
Db 250 IACIGPPNICLDRELTWITSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 309
QY 61 IVELFRNLKMSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 120
Db 310 IVDLFRNLKMSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

RESULT 12
Q6DVF3
ID Q6DVF3 PRELIMINARY; PRT; 765 AA.
AC Q6DVF3
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Signal transducer and activation of transcription factor 3.

OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Belontiiformes; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT46364.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;

Query Match 94.9%; Score 635; DB 2; Length 765;
Best Local Similarity 93.8%; Pred. No. 7e-51;
Matches 121; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRELTWITSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 60
Db 250 IACIGPPNICLDRELTWITSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 309
QY 61 IVELFRNLKMSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 120
Db 310 IVDLFRNLKMSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

RESULT 13
Q6GUE7
ID Q6GUE7 PRELIMINARY; PRT; 785 AA.
AC Q6GUE7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Signal transducer and activator of transcription 3 isoform 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Belontiiformes; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT46364.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;

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DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS5001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F2311BDE27DE398 CRC64;

Query Match          94.9%; Score 635; DB 2; Length 785;
Best Local Similarity 93.8%; Pred. No. 7.2e-51;
Matches 121; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
Db 250 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 309
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYOLKIKVCI 120
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYOLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

RESULT 14
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
[1]
RN SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; IBG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS5001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFEL8BEFD8BE CRC64;

Query Match          93.3%; Score 624; DB 2; Length 764;
Best Local Similarity 92.2%; Pred. No. 7.5e-50;
Matches 119; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
Db 250 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 309
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYOLKIKVCI 120
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYOLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

RESULT 15
O13133 PRELIMINARY; PRT; 767 AA.
AC O13133;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STAT3.
GN Name=rbStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]
RN SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; IBG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match          89.7%; Score 600; DB 2; Length 767;
Best Local Similarity 89.9%; Pred. No. 1.3e-47;
Matches 116; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
Db 250 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 309
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYOLKIKVCI 120
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYOLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

Search completed: May 25, 2005, 17:43:41
Job time : 53.6753 secs
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 51.0983 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-25
Perfect score: 494
Sequence: 1 KLEELQKVSYKGDPIVQH.....LNYQLKIKVICDKSDGVAA 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES-

Result No.	Score	Query Match	Length	DB ID	Description
1	494	100.0	96	4 AAY72857	Aay72857 Mouse Sta
2	494	100.0	129	4 AAY72856	Aay72856 Mouse Sta
3	494	100.0	185	4 AAY72855	Aay72855 Mouse Sta
4	494	100.0	223	4 AAY72854	Aay72854 Mouse Sta
5	494	100.0	271	4 AAY72841	Aay72841 Mouse Sta
6	494	100.0	720	5 AAE22055	Aae22055 Human Sta
7	494	100.0	769	5 ABB57164	Abb57164 Mouse isc
8	494	100.0	769	5 AAE22054	Aae22054 Human Sta
9	494	100.0	769	5 AAE22056	Aae22056 Human pro
10	494	100.0	770	2 AAY72082	Aay72082 Mouse Sta
11	494	100.0	770	2 AAR82995	Aar82995 Mouse liv
12	494	100.0	770	2 AAW03176	Aaw03176 Mouse Sta
13	494	100.0	770	2 AAY03768	Aay03768 Human STA
14	494	100.0	770	3 AAB12377	Aab12377 N-termina
15	494	100.0	770	5 AAE14652	Aae14652 Murine ST
16	494	100.0	770	5 ABG69497	Abg69497 Human bai
17	494	100.0	770	6 ABU10476	Abu10476 Mouse STA
18	494	100.0	770	8 ADN04365	Adn04365 Antipsori
19	494	100.0	770	8 ADP54789	Adp54789 Human PRO
20	494	100.0	793	3 AAB58442	Aab58442 Lung canc
21	491	99.4	770	7 ADD44738	Add44738 Rat Prote
22	489	99.0	770	2 AAR82993	Aar82993 Human pla
23	489	99.0	770	4 AAB19964	Aab19964 Human sig
24	489	99.0	770	5 AAE15174	Aae15174 Human Sta
25	489	99.0	770	7 ADD44740	Add44740 Human Pro

ALIGNMENTS

RESULT 1									
AAY72857									
ID	AAV72857	standard; protein; 96 AA.	228	4	AAV72861	Mouse Sta	228	4	AAV72861
XX	AAV72857;		396	80.2	396	80.2	229	4	AAV72850
AC	AAV72857;		396	80.2	396	80.2	229	4	AAV72863
XX	31-MAY-2001 (first entry)		396	80.2	396	80.2	229	4	AAV72862
XX	Mouse Stat3 protein fragment #15 (282-377 amino acids).		396	80.2	396	80.2	229	4	AAV72862
XX	Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;		396	80.2	396	80.2	229	4	AAV72862
KW	cellular transformation; dysproliferative disease; cancer; psoriasis;		396	80.2	396	80.2	229	4	AAV72862
KW	therapy.		396	80.2	396	80.2	229	4	AAV72862
XX	Mus musculus.		396	80.2	396	80.2	229	4	AAV72862
XX	Key	Location/Qualifiers	396	80.2	396	80.2	229	4	AAV72862
FT	Region	61..77	396	80.2	396	80.2	229	4	AAV72862
FT	/notes= "Stat3-c-Jun interaction region 2; corresponds to		396	80.2	396	80.2	229	4	AAV72862
FT	342-358 position of Stat3 protein"		396	80.2	396	80.2	229	4	AAV72862
XX	WO200116605-A2.		396	80.2	396	80.2	229	4	AAV72862
XX	08-MAR-2001.		396	80.2	396	80.2	229	4	AAV72862
XX	30-AUG-2000; 2000WO-US023822.		396	80.2	396	80.2	229	4	AAV72862
XX	31-AUG-1999; 99US-00387418.		396	80.2	396	80.2	229	4	AAV72862
XX	(UYRQ) UNIV ROCKEFELLER.		396	80.2	396	80.2	229	4	AAV72862
XX	Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;		396	80.2	396	80.2	229	4	AAV72862
XX	WPI; 2001-226705/23.		396	80.2	396	80.2	229	4	AAV72862
XX	Identifying an agent for use in modulating the interaction between		396	80.2	396	80.2	229	4	AAV72862
XX	transcription factor c-Jun and a Stat3 protein.		396	80.2	396	80.2	229	4	AAV72862
XX	Claim 65; Page 81; 86pp; English.		396	80.2	396	80.2	229	4	AAV72862
XX	The present sequence is mouse Stat3 protein fragment containing 282-377		396	80.2	396	80.2	229	4	AAV72862
XX	amino acids of Stat3 protein. The invention relates to methods for		396	80.2	396	80.2	229	4	AAV72862
XX	identifying interacting regions of transcription factors and methods for		396	80.2	396	80.2	229	4	AAV72862
XX	identifying agents which modulates the interaction between a		396	80.2	396	80.2	229	4	AAV72862
XX	transcription factor such as c-Jun and a Stat protein such as Stat-1 and		396	80.2	396	80.2	229	4	AAV72862
XX	Stat-3, useful for modulating gene transcription e.g., cellular		396	80.2	396	80.2	229	4	AAV72862
XX	transformation. These identifying agents are used in the treatment of		396	80.2	396	80.2	229	4	AAV72862
XX	dysproliferative diseases and also for treating cancer and psoriasis. A		396	80.2	396	80.2	229	4	AAV72862

CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 96 AA;

Query Match 100.0%; Score 494; DB 4; Length 96;
 Best Local Similarity 100.0%; Pred. No. 3.6e-55;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMPHDPRLVIKT 60
 DB 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMPHDPRLVIKT 60
 QY 61 GVQFTTKVRLLVKFPPELVQKIKVICDKDGDVAA 96
 DB 61 GVQFTTKVRLLVKFPPELVQKIKVICDKDGDVAA 96

RESULT 2
 AAY72856
 ID AAY72856 standard; protein; 129 AA.
 XX
 AC AAY72856;
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 protein fragment #14 (249-377 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 94..110
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX
 DR Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX
 PS Claim 65; Page 80-81; 86pp; English.

XX The present sequence is mouse Stat3 protein fragment containing 249-377
 CC amino acids of Stat3 protein. The invention relates to methods for
 CC identifying interacting regions of transcription factors and methods for
 CC identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 XX Sequence 129 AA;

Query Match 100.0%; Score 494; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 5.2e-55;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMPHDPRLVIKT 60
 DB 34 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMPHDPRLVIKT 93
 QY 61 GVQFTTKVRLLVKFPPELVQKIKVICDKDGDVAA 96
 DB 94 GVQFTTKVRLLVKFPPELVQKIKVICDKDGDVAA 129

RESULT 3
 AAY72855
 ID AAY72855 standard; protein; 185 AA.
 XX
 AC AAY72855;
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 protein fragment #13 (193-377 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 150..166
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX
 DR Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX
 PS Claim 65; Page 80; 86pp; English.

XX The present sequence is mouse Stat3 protein fragment containing 193-377
 CC amino acids of Stat3 protein. The invention relates to methods for
 CC identifying interacting regions of transcription factors and methods for
 CC identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 XX Sequence 185 AA;

Query Match 100.0%; Score 494; DB 4; Length 185;
 Best Local Similarity 100.0%; Pred. No. 8.4e-55;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMPHDPRLVIKT 60
 DB 90 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMPHDPRLVIKT 149
 QY 61 GVQFTTKVRLLVKFPPELVQKIKVICDKDGDVAA 96

Db 150 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 185
|||||
RESULT 4
AA72854
ID AAY72854 standard; protein; 223 AA.
XX AAY72854;
AC AAY72854;
XX 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #12 (155-377 amino acids).
DE Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX Mus musculus.
XX Key Location/Qualifiers
FT Region 188..204
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX Claim 65; Page 79; 86pp; English.
XX The present sequence is mouse Stat3 protein fragment containing 155-377
CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX Sequence 223 AA;
SQ
Query Match 100.0%; Score 494; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKSAFVVERQPCMPMHPDRPLVIKT 60
Db 128 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKSAFVVERQPCMPMHPDRPLVIKT 187
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 188 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 223
RESULT 5
AA72841
ID AAY72841 standard; protein; 271 AA.
XX AAY72841;
AC AAY72841;
XX 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #2 (107-377 amino acids).
DE Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX Mus musculus.
XX Key Location/Qualifiers
FT Region 24..48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX 236..252
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX Claim 65; Page 67-68; 86pp; English.
XX The present sequence is mouse Stat3 protein fragment containing 107-377
CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
CC to c-Jun protein in the cell extract. The invention relates to methods
CC for identifying interacting regions of transcription factors and methods
CC for identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX Sequence 271 AA;
SQ
Query Match 100.0%; Score 494; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.4e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKSAFVVERQPCMPMHPDRPLVIKT 60
Db 176 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKSAFVVERQPCMPMHPDRPLVIKT 235
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 236 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
RESULT 6
AAE22055
ID AAE22055 standard; protein; 720 AA.
XX AAE22055;
AC AAE22055;
XX

DT 25-JUL-2002 (first entry)
XX Human Stat3beta protein.
DE
XX
KW Human; signal transducer and activator of transcription 3; ischaemia;
KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
KW hypoxia; stroke; angioneogenesis; myocardial infarction; hypoglycaemia;
KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
KW shock; chronic active hepatitis; adult respiratory distress syndrome;
KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
PH Misc-difference 713..714
FT /note= "Encoded by ACA CCA TTC"
FT
XX WO200220032-A1.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028254.
XX
XX 08-SEP-2000; 2000US-0231212P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX (UYSF-) UNIV SOUTH FLORIDA.
XX
XX Yu H, Pardoll D, Jove R, Dalton W;
XX
XX WPI; 2002-362218/39.
XX N-PSDB; AAD35066.
XX
XX Modulating angiogenesis and an immune response in an individual, for
XX treating a hypoxic or ischemic condition, comprises administering a
XX compound that modulates the activity of a signal transducer and activator
XX of transcription 3.
XX
XX Disclosure; Page 87-89; 94pp; English.
XX
XX The invention relates to a method of modulating angiogenesis and immune
XX response. Method involves administering to an individual a compound that
XX modulate the activity of signal transducer and activator of transcription
XX 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
XX hypoxic or ischaemic condition or disorder which is the result of stroke,
XX ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
XX tissue ischaemia in the lower extremities, infarction, trauma, vascular
XX occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
XX chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
XX epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
XX nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
XX with neovascularisation. Suppressing an immune response is useful for
XX ameliorating a symptom of an autoimmune disease such as systemic lupus
XX erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
XX Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
XX mixed connective tissue disease, primary biliary cirrhosis, pernicious
XX anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
XX gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
XX idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
XX disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
XX infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
XX dense deposit disease. The method is useful in preventing or treating
XX specific proliferative and oncogenic disease which includes sarcomas and
XX carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
XX fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
XX hypoproliferative disorders, physical trauma, lesions and wounds. The
XX method is also used in gene therapy. The present sequence is human

CC Stat3beta protein
XX
SQ Sequence 720 AA;

Query Match 100.0%; Score 494; DB 5; Length 720;
Best Local Similarity 100.0%; Pred. No. 4.8e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLLEELQOKVSVKGGDPVQHRPMLERIVLELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
DB 282 KKLLEELQOKVSVKGGDPVQHRPMLERIVLELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVICDKSGDVAA 96
DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVICDKSGDVAA 377

RESULT 7
ABB57164
ID ABB57164 standard; protein; 769 AA.
XX
XX ABB57164;
AC
XX
DT 07-MAR-2002 (first entry)
XX
XX Mouse ischaemic condition related protein sequence SEQ ID NO:398.
DE
XX
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
XX Mus musculus.
XX
XX WO20018188-A2.
PN
XX
XX 22-NOV-2001.
PD
XX
XX 18-MAY-2001; 2001WO-JP004192.
PF
XX
XX 18-MAY-2000; 2000JP-00145977.
PR
XX
XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
PA
XX
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
PI
XX
XX WPI; 2002-034733/04.
DR
XX N-PSDB; ABI99454.
DR
XX
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
XX Claim 2; Page 1084-1087; 2690pp; English.
PS
XX
XX The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
XX
SQ Sequence 769 AA;

Query Match 100.0%; Score 494; DB 5; Length 769;
Best Local Similarity 100.0%; Pred. No. 5.3e-54;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKEELQKQVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KKEELQKQVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVOFTTKVRLLVKFPPELVQKIKVCIDKDSGDVAA 96
 DB 342 GVOFTTKVRLLVKFPPELVQKIKVCIDKDSGDVAA 377

RESULT 8
 AAE22054
 ID AAE22054 standard; protein; 769 AA.
 XX
 AC AAE22054;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Human Stat3 protein.
 XX
 KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 XX
 OS Homo sapiens.
 XX
 PN WO200220032-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028254.
 XX
 PR 08-SEP-2000; 2000US-0231212P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Yu H, Pardoll D, Jove R, Dalton W;
 XX
 DR WPI; 2002-362218/39.
 DR N-PSDB; AAD35065.
 XX
 PT Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX
 PS Disclosure; Page 83-85; 94pp; English.
 XX
 CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,

CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neuropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein
 XX
 SQ Sequence 769 AA;

Query Match 100.0%; Score 494; DB 5; Length 769;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKEELQKQVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KKEELQKQVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVOFTTKVRLLVKFPPELVQKIKVCIDKDSGDVAA 96
 DB 342 GVOFTTKVRLLVKFPPELVQKIKVCIDKDSGDVAA 377

RESULT 9
 AAE22056
 ID AAE22056 standard; protein; 769 AA.
 XX
 AC AAE22056;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Human protein related to angiogenesis regulation.
 XX
 KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 XX
 OS Homo sapiens.
 XX
 PN WO200220032-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028254.
 XX
 PR 08-SEP-2000; 2000US-0231212P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Yu H, Pardoll D, Jove R, Dalton W;
 XX
 DR WPI; 2002-362218/39.
 DR N-PSDB; AAD35065.
 XX
 PT Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.

PT of transcription 3.
 PS Disclosure; Page 83-85; 94pp; English.
 XX
 CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epileps, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation
 XX
 SQ Sequence 769 AA;

Query Match 100.0%; Score 494; DB 5; Length 769;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVQFTTKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 DB 342 GVQFTTKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 10
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX
 AC AAR72082;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX
 XX Mouse Stat3 (19sf6).
 XX
 KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX
 OS Mus sp.
 XX
 PN W09508629-A1.
 XX
 PD 30-MAR-1995.
 XX
 XX 26-SEP-1994; 94WO-US010849.
 XX
 PF 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126595.

PR 11-MAR-1994; 94US-00212184.
 PR 11-MAR-1994; 94US-00212185.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 XX WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 DR
 XX Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX
 PS Claim 1; Page 107-110; 160pp; English.
 XX
 CC A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 494; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVQFTTKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 DB 342 GVQFTTKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 11
 AAR82995
 ID AAR82995 standard; protein; 770 AA.
 XX
 AC AAR82995;
 XX
 XX 25-MAR-1996 (first entry)
 DT
 XX Mouse liver acute phase response factor.
 DE
 XX Mouse; acute phase response factor; transcription factor; interleukin-6;
 KW signal transduction; liver; antibody; antitumor; hypotensive; therapy.
 KW antiinflammatory; antitumor; hypotensive; therapy.
 XX
 OS Mus musculus.
 XX
 PN EP676469-A2.
 XX
 PD 11-OCT-1995.
 XX
 PF 29-MAR-1995; 95BP-00104670.
 XX
 XX 04-APR-1994; 94JP-00065825.
 XX
 PA (KISH/) KISHIMOTO T.
 XX
 PI Akira S, Kishimoto T;
 XX WPI; 1995-346089/45.
 DR N-PSDB; AAT05619.
 XX
 PT New acute phase response factor - for developing inhibitory agents for

PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
 PT diseases.

PS Claim 10; Page 20-22; 31pp; English.

XX The sequence represents a mouse acute phase response factor (APRF), a
 CC transcription factor related to signal transmission of interleukin-6 (IL-
 CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
 CC library using a polymerase chain reaction product (amplified using
 CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
 CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
 CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
 CC inflammatory disease, leukemia, cancer, osteoclastia, pulmonary
 CC hypertension, etc

XX SQ Sequence 770 AA;

Query Match 100.0%; Score 494; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPMPHDPRLVIKT 60
 DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPMPHDPRLVIKT 341

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 DB 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 12

AAW03176
 ID AAW03176 standard; protein; 770 AA.

AC AAW03176;

DT 24-OCT-1996 (first entry)

XX Mouse STAT4.

KW STAT; STAT4; signal transducer and activator of transcription;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW autoimmune disease; antagonist; therapy.

XX Mus sp.

EH Key Location/Qualifiers
 FT Domain 398..508
 FT /label= DNA_binding_domain
 FT /note= "Claim 3, page 110"

XX WO9620954-A2.

XX 11-JUL-1996.

XX 28-DEC-1995; 95WO-US017025.

XX 06-JAN-1995; 95US-00369796.

XX (UYRQ) UNIV ROCKEFELLER.

XX Darnell JE, Wen Z, Horvath CM, Zhong Z;

XX WPI; 1996-333941/33.

XX N-PSDB; AAT31280.

XX New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
 PT preventing or treating cellular dysfunction, e.g. oncogenesis,
 PT inflammation, parasitic disease or autoimmunity.

XX Disclosure; Page 87-90; 138pp; English.

XX Mouse signal transducer and activator of transcription (STAT) protein

CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
 CC ligand-activated receptor kinase complexes followed by nuclear
 CC translocation and DNA binding to activate transcription. Recombinant
 CC STAT4 can be obtd. using cDNA clone 19af6 (AAT31278) obtd. from
 CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
 CC AAW03167) capable of both receptor recognition and message delivery via
 CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
 CC DNA binding domains (see also AAW03165-75) are useful for screening
 CC antagonists used to inhibit STAT-mediated signal transduction and
 CC activation of transcription

XX SQ Sequence 770 AA;

Query Match 100.0%; Score 494; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPMPHDPRLVIKT 60
 DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPMPHDPRLVIKT 341

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 DB 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 13

AAV03768

ID AAV03768 standard; protein; 770 AA.

AC AAV03768;

DT 11-JUN-1999 (first entry)

XX Human STAT3 allelic variant.

KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
 KW intracellular transcription factor; interleukin-6; medicament; variant;
 KW pharmaceutical; autoimmune disease; inflammatory; human.

XX Homo sapiens.

XX EP905234-A2.

XX 31-MAR-1999.

XX 18-FEB-1998; 98EP-00102774.

XX 16-SEP-1997; 97EP-00116061.

XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Serlupi-Crescenzi O, Della Pietra L;

XX WPI; 1999-192664/17.

XX N-PSDB; AAX29281.

XX New human Signal Transducer and Activator of Transcription 3 (STAT3)
 PT allelic variant useful for treatment of autoimmune and inflammatory
 PT disease.

XX Claim 2; Page 9-13; 32pp; English.

XX The present sequence represents a predominant allelic variant of human
 CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
 CC intracellular transcription factor which mediates IL-6 signals. The
 CC encoding sequence differs from the original published human STAT3 gene
 CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
 CC DNA molecule can be used for the recombinant expression of the variant.
 CC STAT3 protein is useful as a medicament or pharmaceutical composition for
 CC treatment of autoimmune or inflammatory diseases

XX SQ Sequence 770 AA;

Query Match 100.0%; Score 494; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKT 60
 DB 282 KKEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKT 341
 QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 14
 AAB12377
 ID AAB12377 standard; peptide; 770 AA.
 XX
 AC AAB12377;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE N-terminal domain of murine STAT-3 protein.
 XX
 KW STAT; signal transducer and activator of transcription; crystal;
 KW drug design; murine.
 XX
 OS Mus sp.

Key	Region	Location/Qualifiers
FT	Region	4..9
FT	Region	/label= Alpha helix 1
FT	Region	12..21
FT	Region	/label= Alpha helix 2
FT	Region	19..21
FT	Region	/label= 3(10) helix of alpha helix 2
FT	Region	28..33
FT	Region	/label= Alpha helix 3
FT	Region	35..40
FT	Region	/label= Alpha helix 4
FT	Region	43..47
FT	Region	/label= Alpha helix 5
FT	Region	50..73
FT	Region	/label= Alpha helix 6
FT	Region	77..96
FT	Region	/label= Alpha helix 7
FT	Region	99..119
FT	Region	/label= Alpha helix 8

US6087478-A.
 11-JUL-2000.
 23-JAN-1998; 98US-00012710.
 23-JAN-1998; 98US-00012710.
 (UYRQ) UNIV ROCKEFELLER.
 Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
 WPI; 2000-505108/45.

New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
 Disclosure; Fig 1; 42pp; English.

The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater

than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structural structure determined for the crystal

Sequence 770 AA;

Query Match 100.0%; Score 494; DB 3; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKT 60
 DB 282 KKEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKT 341
 QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 15
 AAE14652
 ID AAE14652 standard; protein; 770 AA.
 XX
 AC AAE14652;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE Murine STAT3 protein.
 XX
 KW Signal transducer and activator of transcription; STAT3;
 KW drug development; drug discovery; crystal; inflammation; allergy; asthma;
 KW leukaemia; anaemia; neutropenia; thrombocytopaenia; cancer; obesity;
 KW viral disease; growth retardation; murine.
 XX
 OS Mus sp.

Key	Domain	Location/Qualifiers
FT	Domain	1..130
FT	Domain	/note= "Conserved N-terminal domain of the STAT family"

US6312887-B1.

06-NOV-2001.

24-APR-2000; 2000US-00556273.

23-JAN-1998; 98US-00012710.

(UYRQ) UNIV ROCKEFELLER.

Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;

WPI; 2002-033337/04.

Identifying compounds that bind to signal transducer and activator of transcription proteins, useful for the production of new drugs.

Example; Col 47-50; 44pp; English.

The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein, identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new

CC drugs. An antagonist of STAT N-terminal dimeric interactions that
CC inhibits the binding of the STAT dimers to adjacent weak binding sites on
CC a promoter of a gene, could be useful as drugs in the treatment of
CC diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other
CC hand, an agonist of N-terminal dimeric interactions between STAT dimers,
CC can be used as drugs in the treatment of diseases e.g. anaemia,
CC neutropenia, thrombocytopaenia, cancer, obesity, viral diseases and
CC growth retardation. The present sequence is murine STAT3 protein
XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 494; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.3e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGLEELQKQVSYKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKT 60
|||
Db 282 KGLEELQKQVSYKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKT 341
|||

Qy 61 GVQFTTKVRLLVKPPPELNYQLKIKVCIDKDSGDVAA 96
|||
Db 342 GVQFTTKVRLLVKPPPELNYQLKIKVCIDKDSGDVAA 377
|||

Search completed: May 25, 2005, 17:36:36
Job time : 51.265 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 12.0119 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-25
Perfect score: 494
Sequence: 1 KXLEELQOKVSYKGDPIVQH.....LNYQLKIKVICDKSGDVAA 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	494	100.0	96	3	US-09-387-418A-25
2	494	100.0	129	3	US-09-387-418A-24
3	494	100.0	185	3	US-09-387-418A-23
4	494	100.0	223	3	US-09-387-418A-22
5	494	100.0	271	3	US-09-387-418A-9
6	494	100.0	770	1	US-08-369-796-12
7	494	100.0	770	1	US-08-416-581B-9
8	494	100.0	770	2	US-08-852-091-12
9	494	100.0	770	2	US-08-820-754-12
10	494	100.0	770	3	US-08-956-652-12
11	494	100.0	770	3	US-08-956-869-12
12	494	100.0	770	3	US-09-012-710-8
13	494	100.0	770	3	US-08-948-547-12
14	494	100.0	770	3	US-09-364-970-3
15	494	100.0	770	3	US-09-364-970-5
16	494	100.0	770	3	US-09-556-273-8
17	494	100.0	770	3	US-08-956-653A-12
18	494	100.0	770	3	US-09-526-542-2
19	494	100.0	770	4	US-08-212-185-12
20	494	100.0	770	4	US-10-117-087-2
21	494	100.0	770	5	PCT-US95-17025-12
22	489	99.0	770	1	US-08-416-581B-1
23	489	99.0	770	1	US-08-416-581B-5
24	489	99.0	770	3	US-09-087-465-6
25	489	99.0	770	4	US-09-372-800A-6
26	489	99.0	771	1	US-08-276-099A-14
27	489	99.0	771	1	US-08-781-890-14

28	396	80.2	229	3	US-09-387-418A-18	Sequence 18, Appl
29	396	80.2	229	3	US-09-387-418A-28	Sequence 28, Appl
30	396	80.2	229	3	US-09-387-418A-30	Sequence 30, Appl
31	396	80.2	229	3	US-09-387-418A-31	Sequence 31, Appl
32	396	80.2	252	3	US-09-387-418A-14	Sequence 14, Appl
33	379	76.7	229	3	US-09-387-418A-29	Sequence 29, Appl
34	318	64.4	213	3	US-09-387-418A-19	Sequence 19, Appl
35	318	64.4	236	3	US-09-387-418A-15	Sequence 15, Appl
36	310	62.8	268	3	US-09-387-418A-12	Sequence 12, Appl
37	310	62.8	592	4	US-09-430-806A-3	Sequence 3, Appl
38	310	62.8	712	1	US-08-369-796-6	Sequence 6, Appl
39	310	62.8	712	2	US-08-852-091-6	Sequence 6, Appl
40	310	62.8	712	2	US-08-820-754-6	Sequence 6, Appl
41	310	62.8	712	3	US-08-956-652-6	Sequence 6, Appl
42	310	62.8	712	3	US-08-956-869-6	Sequence 6, Appl
43	310	62.8	712	3	US-08-948-547-6	Sequence 6, Appl
44	310	62.8	712	3	US-08-956-653A-6	Sequence 6, Appl
45	310	62.8	712	4	US-08-212-185-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-387-418A-25
; Sequence 25, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melisea H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-25

Query Match		100.0%;	Score 494;	DB 3;	Length 96;
Best Local Similarity		100.0%;	Pred. No. 4.3e-54;		
Matches	96;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1	KXLEELQOKVSYKGDPIVQHRPMLERIIVELFRLMKSAFVVERQPCMPMHPDRPLVIKT	60		
Db	1	KXLEELQOKVSYKGDPIVQHRPMLERIIVELFRLMKSAFVVERQPCMPMHPDRPLVIKT	60		
QY	61	GVQFTTKVRLLYKFPPELNYQLKIKVICDKSGDVAA	96		
Db	61	GVQFTTKVRLLYKFPPELNYQLKIKVICDKSGDVAA	96		

RESULT 2
US-09-387-418A-24
; Sequence 24, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melisea H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-24

Query Match      100.0%; Score 494; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 6.3e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPTVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
    |||||||
Db 34 KLEELQOKVSYKGDPTVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 93
    |||||||

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
    |||||||
Db 94 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 129
    |||||||

RESULT 3
US-09-387-418A-23
; Sequence 23, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-23

Query Match      100.0%; Score 494; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPTVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
    |||||||
Db 90 KLEELQOKVSYKGDPTVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 149
    |||||||

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
    |||||||
Db 150 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 185
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RESULT 4
US-09-387-418A-22
; Sequence 22, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 223
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-22

Query Match      100.0%; Score 494; DB 3; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPTVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
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Db 128 KLEELQOKVSYKGDPTVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 187
    |||||||

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
    |||||||
Db 188 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 223
    |||||||

RESULT 5
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match      100.0%; Score 494; DB 3; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.7e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPTVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
    |||||||
Db 176 KLEELQOKVSYKGDPTVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 235
    |||||||

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
    |||||||
Db 236 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
    |||||||

RESULT 6
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-369-796-12

Query Match 100.0%; Score 494; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKEELQKQVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLVIKT 60
DB 282 KKEELQKQVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLVIKT 341
QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 96
DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 7
US-08-416-581B-9
Sequence 9, Application US/08416581B
Patent No. 5719042
GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-37891
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-416-581B-9
Query Match 100.0%; Score 494; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKEELQKQVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLVIKT 60
DB 282 KKEELQKQVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLVIKT 341
QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 96
DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 8
US-08-852-091-12
Sequence 12, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-091-12

Query Match 100.0%; Score 494; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 282 KKEELQKQVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLVIKT 341

QY 61 GVOFTTKVRLVKFPELNYQLKIKVCIDKDSGDVAA 96
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RESULT 9
 US-08-820-754-12
 ; Sequence 12, Application US/08820754
 ; Patent No. 5976835
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zhong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/820,754
 ; FILING DATE: 19-MAR-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-820-754-12

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 Best Local Similarity 100.0%; Pred. No. 6.4e-53;
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 QY 1 KLEELQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
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 Db 282 KLEELQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 341

QY 61 GVOFTTKVRLVKFPELNYQLKIKVCIDKDSGDVAA 96
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 Db 342 GVOFTTKVRLVKFPELNYQLKIKVCIDKDSGDVAA 377

RESULT 10
 US-08-956-652-12
 ; Sequence 12, Application US/08956652
 ; Patent No. 6013475
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zhong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/956,652
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-956-652-12

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 Db 282 KLEELQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 341
 QY 61 GVOFTTKVRLVKFPELNYQLKIKVCIDKDSGDVAA 96

Db 342 GVQFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 377

RESULT 11
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-869-12

Query Match 100.0%; Score 494; DB 3; Length 770;
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Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 282 KXLEELQKVSXGDPVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLVIKT 341
QY 61 GVQFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 377

RESULT 12
US-09-012-710-8
; Sequence 8, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-012-710-8
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Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 282 KXLEELQKVSXGDPVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLVIKT 341
QY 61 GVQFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 377

RESULT 13
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: IBM PC compatible
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; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-948-547-12

Query Match 100.0%; Score 494; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLEELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 14
US-09-364-970-3
; Sequence 3, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-364-970-5

Query Match 100.0%; Score 494; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLEELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KKLEELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 341

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	494	100.0	129	13	Sequence 25, Appl
3	494	100.0	185	13	Sequence 24, Appl
4	494	100.0	223	13	US-10-090-185-23
5	494	100.0	271	13	Sequence 22, Appl
6	494	100.0	720	15	US-10-090-185-22
7	494	100.0	769	15	Sequence 9, Appl
8	494	100.0	769	15	US-10-380-020-2
9	494	100.0	770	11	US-10-380-020-5
10	494	100.0	770	14	US-09-876-773-12
11	494	100.0	770	14	US-10-045-792-8
12	494	100.0	770	14	US-10-038-010-56
13	494	100.0	770	14	US-10-117-087-2
			770	17	US-10-639-617-12

14	494	100.0	793	9	US-09-925-302-780	Sequence 780, App
15	494	100.0	793	10	US-09-925-302-780	Sequence 780, App
16	491	99.4	770	15	US-10-116-275-329	Sequence 329, App
17	489	99.0	770	15	US-10-116-275-349	Sequence 349, App
18	396	80.2	229	13	US-10-090-185-18	Sequence 18, Appl
19	396	80.2	229	13	US-10-090-185-28	Sequence 28, Appl
20	396	80.2	229	13	US-10-090-185-30	Sequence 30, Appl
21	396	80.2	229	13	US-10-090-185-31	Sequence 31, Appl
22	396	80.2	252	13	US-10-090-185-14	Sequence 14, Appl
23	379	76.7	229	13	US-10-090-185-29	Sequence 29, Appl
24	318	64.4	213	13	US-10-090-185-19	Sequence 19, Appl
25	318	64.4	236	13	US-10-090-185-15	Sequence 15, Appl
26	311	63.0	749	9	US-09-833-205-4	Sequence 4, Appl
27	310	62.8	268	13	US-10-090-185-12	Sequence 12, Appl
28	310	62.8	582	14	US-10-245-120-3	Sequence 3, Appl
29	310	62.8	712	11	US-09-876-773-6	Sequence 6, Appl
30	310	62.8	712	14	US-10-245-120-2	Sequence 2, Appl
31	310	62.8	712	17	US-10-639-617-6	Sequence 6, Appl
32	310	62.8	712	17	US-10-936-390-5	Sequence 5, Appl
33	310	62.8	750	9	US-09-833-205-2	Sequence 2, Appl
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35	310	62.8	750	14	US-10-245-120-1	Sequence 1, Appl
36	310	62.8	750	14	US-10-308-279-44	Sequence 44, Appl
37	310	62.8	750	16	US-10-755-889-352	Sequence 352, App
38	310	62.8	750	16	US-10-755-889-823	Sequence 823, App
39	310	62.8	750	17	US-10-492-043-19	Sequence 19, Appl
40	310	62.8	750	17	US-10-639-617-4	Sequence 4, Appl
41	310	62.8	786	9	US-09-925-297-550	Sequence 550, App
42	291	58.9	423	14	US-10-177-293-437	Sequence 437, App
43	291	58.9	748	14	US-10-177-293-439	Sequence 439, App
44	231	58.9	748	16	US-10-755-889-70	Sequence 70, Appl
45	291	58.9	748	16	US-10-755-889-362	Sequence 362, App

ALIGNMENTS

RESULT 1

US-10-090-185-25
; Sequence 25, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-25

Query Match	100.0%;	Score	494;	DB	13;	Length	96;
Best Local Similarity	100.0%;	Pred. No.	2.9e-53;				
Matches	96;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
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Qy	61	GVQFTTKVLLVKFPPLNYQLKVICDKSGDVAA	96				
Db	61	GVQFTTKVLLVKFPPLNYQLKVICDKSGDVAA	96				

RESULT 2

US-10-090-185-24
; Sequence 24, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-24

Query Match 100.0%; Score 494; DB 13; Length 129;

Best Local Similarity 100.0%; Pred. No. 4.2e-53; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0;

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Db 34 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 93

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96

Db 94 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 129

RESULT 3

US-10-090-185-23
; Sequence 23, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-23

Query Match 100.0%; Score 494; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 6.7e-53; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60

Db 90 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 149

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96

Db 150 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 185

RESULT 4

US-10-090-185-22
; Sequence 22, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-22

Query Match 100.0%; Score 494; DB 13; Length 223;

Best Local Similarity 100.0%; Pred. No. 8.5e-53; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60

Db 128 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 187

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96

Db 188 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 223

RESULT 5

US-10-090-185-9
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-9

Query Match 100.0%; Score 494; DB 13; Length 271;

Best Local Similarity 100.0%; Pred. No. 1.1e-52; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60

Db 176 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 235

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96

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1  RESULT 9
2  US-09-876-773-12
3  ; Sequence 12, Application US/09876773
4  ; Publication No. US20040058318A1
5  GENERAL INFORMATION:
6  APPLICANT: Darnell Jr., James E.
7  ;
8  ; Schindler, Christian W.
9  ; Fu, Xian-Yuan
10 ; Wen, Zilong
11 ;
12 ; Zhong, Zhong
13 ;
14 TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
15 ; SEQUENCES AND METHODS OF USE THEREOF
16 ;
17 NUMBER OF SEQUENCES: 25
18 ;
19 CORRESPONDENCE ADDRESS:
20 ;
21 ADDRESSEE: Klauber & Jackson
22 ;
23 STREET: 411 Hackensack Avenue
24 ; CITY: Hackensack
25 ; STATE: New Jersey
26 ; COUNTRY: USA
27 ; ZIP: 07601
28 ;
29 COMPUTER READABLE FORM:
30 ; MEDIUM TYPE: Floppy disk
31 ; COMPUTER: IBM PC compatible
32 ; OPERATING SYSTEM: PC-DOS/MS-DOS
33 ; SOFTWARE: Patent In Release #1.0, Version #1.25
34 CURRENT APPLICATION DATA:
35 ; APPLICATION NUMBER: US/09/876,773
36 ; FILING DATE: 07-Jun-2001
37 ; CLASSIFICATION: 435
38 ;
39 PRIOR APPLICATION DATA:
40 ; APPLICATION NUMBER: US/08/212,185
41 ; FILING DATE: 11-MAR-1994
42 ; APPLICATION NUMBER: US 07/980,498
43 ; FILING DATE: 23-NOV-1992
44 ; APPLICATION NUMBER: US 07/854,296

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FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12
Query Match 100.0%; Score 494; DB 11; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
DB 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377
RESULT 10
US-10-045-792-8
Sequence 8, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8
Query Match 100.0%; Score 494; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
DB 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377
RESULT 11
US-10-038-010-56
Sequence 56, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56
LENGTH: 770
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: STAT3 : Transcription factor
LOCATION: (1)..(770)
OTHER INFORMATION:
US-10-038-010-56
Query Match 100.0%; Score 494; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
DB 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377
RESULT 12
US-10-117-087-2
Sequence 2, Application US/10117087
Publication No. US20030166854A1
GENERAL INFORMATION:
APPLICANT: SERLUPI-CRESCENZI, Ottaviano
APPLICANT: DELLA PIETRA, Linda
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REFERENCE: SERLUPI=2
CURRENT APPLICATION NUMBER: US/10/117,087

; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2

Query Match 100.0%; Score 494; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 341

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 13
US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/639,617
; FILING DATE: 12-Aug-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 100.0%; Score 494; DB 17; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 341

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 14
US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match 100.0%; Score 494; DB 9; Length 793;
Best Local Similarity 100.0%; Pred. No. 4.3e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 305 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 364

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 365 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 400

RESULT 15
US-09-925-302-780
; Sequence 780, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780

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; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match      100.0%; Score 494; DB 10; Length 793;
Best Local Similarity 100.0%; Pred. No. 4.3e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GVQFTTKVRLVLPPELNYQLKIKVCIDKDSGDVAA 96
Db 365 GVQFTTKVRLVLPPELNYQLKIKVCIDKDSGDVAA 400
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Job time : 43.375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: May 25, 2005, 17:24:07 ; Search time 9.0566 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-25
Perfect score: 494
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	494	100.0	770	2 I49508	ISGF3 p91-related
2	489	99.0	770	2 A54444	DNA-binding protein
3	310	62.8	739	2 A46159	interferon-depende
4	283	57.3	748	2 A56047	gamma-interferon a
5	204	41.3	851	2 A46160	interferon alpha-1
6	90.5	18.3	848	2 A54740	interleukin-4-indu
7	86.5	17.5	786	2 I49274	mammary gland fact
8	86.5	17.5	793	2 S54772	mammary gland fact
9	86.5	17.5	794	2 G02317	transcription acti
10	86.5	17.5	794	2 S55527	mammary gland fact
11	83.5	16.9	837	2 I57557	DNA-Binding Protei
12	72	14.6	393	2 S32458	4-hydroxyphenylpyr
13	72	14.6	393	2 S32821	4-hydroxyphenylpyr
14	71	14.4	498	2 T06667	argininosuccinate
15	68	13.8	363	2 S48483	MRS1 protein - yea
16	68	13.8	590	2 A48461	ovarian abundant m
17	68	13.8	1152	2 E71667	2-acylglycerolphosp
18	67	13.6	376	2 S32820	allotigen F - ra
19	67	13.6	402	2 T29703	C kinase 1 interrac
20	67	13.6	415	2 JCT167	fatty-acid-CoA lig
21	67	13.6	508	2 AF1479	F protein - mouse
22	66	13.4	376	2 A60236	hypothetical prote
23	66	13.4	393	2 T25063	fatty-acid-CoA lig
24	66	13.4	508	2 AC1119	complex I intermed
25	65.5	13.3	748	2 T47250	hypothetical prote
26	65.5	13.3	926	2 T39082	hypothetical prote
27	64	13.0	334	1 DEBYMM	malate dehydrogena
28	64	13.0	364	2 T30084	hypothetical prote
29	64	13.0	460	2 H89907	hypothetical prote

30	63.5	12.9	395	2 T43892	translation elonga
31	63	12.8	416	2 A56486	perinuclear bindin
32	63	12.8	695	2 T39954	probable gtpase ac
33	62.5	12.7	339	2 T41126	meiotic recombina
34	62.5	12.7	378	1 S42088	mevalonate kinase
35	62.5	12.7	781	2 T39373	dynamain-related pr
36	62.5	12.7	804	2 B84389	ribonucleoside pr
37	62	12.6	307	1 PNB5L	beta-lactamase (EC
38	62	12.6	328	2 A99345	conserved hypothet
39	62	12.6	369	2 T21556	hypothetical prote
40	62	12.6	580	2 C71182	probable ABC trans
41	62	12.6	1493	2 A38218	GAP-associated pro
42	61.5	12.4	191	2 B70042	hypothetical prote
43	61.5	12.4	256	2 T48076	60S RIBOSOMAL PROT
44	61.5	12.4	451	2 S73433	pre-B cell enhanci
45	61.5	12.4	451	2 B81056	proteinase, probab

ALIGNMENTS

RESULT 1

I49508
ISGF3 p91-related transcription factor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49508; I49009
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr
A;Reference number: A54444, MUID:94208062; PMID:7512451
A;Accession: I49508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P42227; GB:L29278; NID:9476715; PIDN:AAA37254.1; PID:947671
R;Raz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
A;Title: Acute phase response factor and additional members of the interferon-stimulate
A;Reference number: I49009; MUID:95014185; PMID:7523373
A;Accession: I49009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-393, 'M', 395-700, 702-770 <RE2>

A;Cross-references: EMBL:U08378; NID:9473889; PIDN:AAA56668.1; PID:9473890
C;Genetics:
A;Gene: APRF
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 100.0%; Score 494; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-46;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXLEELQQRVSYKGDPIVQHPRMPEERIVELFRNLKSAFVVERQCPMPHPDPLVIKT 60
Db 282 KXLEELQQRVSYKGDPIVQHPRMPEERIVELFRNLKSAFVVERQCPMPHPDPLVIKT 341
|||||

QY 61 GVQFTTKVRLLVKFPPELNYQLKVICDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKVICDKSGDVAA 377
|||||

RESULT 2

A54444
DNA-binding protein APRF - human
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A54444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444

A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:G475788; PID:G475789
C;Genetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor

Query Match 99.0%; Score 489; DB 2; Length 770;
Best Local Similarity 99.0%; Pred. No. 1.6e-45;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 341
Qy 61 GVQFTTKVRLLVKPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKPELNYQLKIKVCIDKSGDVAA 377

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91- and 84-kDa ISGF-3 subunits
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBI:P:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 62.8%; Score 310; DB 2; Length 739;
Best Local Similarity 64.4%; Pred. No. 6.6e-26;
Matches 58; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

Qy 1 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 267 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 326
Qy 61 GVQFTTKVRLLVKPELNYQLKIKVCIDK 90
Db 327 GVQFTTKVRLLVKPELNYQLKIKVCIDK 356

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, M.; Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in esophageal carcinoma cells
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:G509502; PIDN:AAA19692.1; PID:G509503
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 57.3%; Score 283; DB 2; Length 748;
Best Local Similarity 58.9%; Pred. No. 6.1e-23;
Matches 53; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

Qy 1 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 277 EKLEEQSTKWTYBGDPIPAQRAHLERATFLIYNLFKNSFVVERQPCMPMHPDRPLVIKT 336
Qy 61 GVQFTTKVRLLVKPELNYQLKIKVCIDK 90
Db 337 LIQFTVKRLRLVLPYQVVKASIDKN 366

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
N;Alternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA; protein
A;Residues: 1-851 <FUL>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBI:P:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
submitted to the EMBL data library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:G1293919; PIDN:AAA98760.1; PID:G1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in the genome
A;Reference number: S53873; MUID:95192056; PMID:7885841
A;Accession: S53873
A;Status: nucleic acid sequence not shown
A:Molecule type: DNA
A;Residues: 1-196;392-591;684-730 <YAW>
A;Cross-references: EMBL:U18671
C;Genetics:
A;Gene: stat2
A;Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 4
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: signal transduction; transcription regulation

Query Match 41.3%; Score 204; DB 2; Length 851;
Best Local Similarity 44.4%; Pred. No. 3.3e-14;
Matches 40; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

Qy 1 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 277 KEULGSLVSYQDDPLTKGVLDLNAQVTELLQHLHRAVETQPCMPMHPDRPLVIKT 336
Qy 61 GVQFTTKVRLLVKPELNYQLKIKVCIDK 90
Db 337 GSKFTVTRTLVRLQGNESLTVESIDRN 366

RESULT 6
A54740
interleukin-4-induced transcription factor stat - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54740
R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.

Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID: 94367369; PMID:8085155
A;Accession: A54740
A;Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-848 <HOU>
A:Cross-references: UNIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription regulation

Query Match 18.3%; Score 90.5; DB 2; Length 848;
Best Local Similarity 36.2%; Pred.No. 0.091;
Matches 25; Conservative 12; Mismatches 23; Indels 9; Gaps 2;

QY 5 ELQQVSYKGDPT-VQHPRMLEERIVFLFNLMKSFAFVERPCMPMHPDRPLVIKTGVQ 63
DB 237 QLQVEGCAAGGELEPKTRASLTGLDEVLRTLVTSCELFVEKP-----PQLVKTYTQ 288
:
| | | :
| | | :
| | | :

QY 64 FTTKVRLVV 72
DB 289 FQAGVRLLV 297
:
| | | :
| | | :

RESULT 7
I49274
mammary gland factor - mouse
N;Alternate names: STAT5 protein homolog p80
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49274; S54773; S54727
R;Lin, X.; Robinson, G.W.; Guillelleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved i
A;Reference number: I49273; MUID: 96004632; PMID: 7568026
A;Accession: I49274
A;Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: mRNA
A:Residues: 1-786 <RES>
A;Cross-references: UNIPROT:P42233; UNIPROT-Q9JRM1; EMBL:U21110; NID:g747573; PIDN:AACS5
R;Mai, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleuki
A;Reference number: S54772; MUID: 95237198; PMID: 7720707
A;Accession: S54773
A;Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-432, 'E', 434-786 <MU>
A;Cross-references: EMBL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R;Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quella, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID: 95246733; PMID: 7537213
A;Accession: S54727
A;Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-432, 'E', 434-786 <AZA>
C;Genetics:
A;Gene: Stat5B
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 17.5%; Score 86.5; DB 2; Length 786;
Best Local Similarity 30.6%; Pred.No. 0.23;
Matches 22; Conservative 15; Mismatches 26; Indels 9; Gaps 2;

QY 1 KKLFEELQOKSVYSKDPTVOHRPMLEERISVELFNLMKSFAFVERPCMPMHPDRPLVIKT 60
DB 294 RRAHLCCOOLPIPG-PVEEMLAENVATITDIISALVTSTFIIEKP-----PQLVKT 344
:
| | | :
| | | :
| | | :

QY 61 GVQFTTKVRLVV 72
DB 345 QTKFAATVRLVV 356
:
| | | :
| | | :


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          : : | : : : : | : | : | : |
Db      306 AKIRVXESINDVLEELKILVDYDEKGYLLQI 335

RESULT 14
T06667
argininosuccinate synthase (EC 6.3.4.5) - Arabidopsis thaliana
N/Alternate names: protein F617.40
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
C/Accession: T06667
R/Bevan, M.; Terry, N.; Ardiles, W.; Buysschaert, C.; Dasseville, R.; De Clerck, R.; De
oiseil, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1999
A/Reference number: Z15792
A/Accession: T06667
A/Molecule type: DNA
A/Residues: 1-498 <BEV>
A/Cross-references: EMBL:AL049657; GSPDB:GNO0062; ATSP:F617.40
A/Experimental source: cultivar Columbia; BAC clone F617
C/Genetics:
A/Gene: ATSP:F617.40
A/Map position: 4
A/Introns: 25/1; 100/1; 146/2; 162/3; 223/3; 285/3; 315/2
C/Superfamily: argininosuccinate synthase
C/Keywords: ligase

Query Match          14.4%; Score 71; DB 2; Length 498;
Best Local Similarity 25.3%; Pred. No. 6.7;
Matches 21; Conservative 18; Mismatches 36; Indels 8; Gaps 1;

QY      1 KXLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQCPMPHDPRLVIKT 60
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      165 KELEGLEQKAKASGASOLVVKDLTEBFVKDIFPCLRAGAIYERKYLGTSMARPI--- 221

QY      61 GVQFTTKVRLLVKFPPELNYQLKI 83
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      222 -----AKVRPELTFPSLNPELKV 239

RESULT 15
S48483
MRS1 protein - yeast (Saccharomycetes cerevisiae)
N/Alternate names: protein YIR021w
C/Species: Saccharomycetes cerevisiae
C/Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C/Accession: S48483; A29684
R/Rowley, K.
submitted to the EMBL Data Library, October 1994
A/Reference number: S48478
A/Accession: S48483
A/Molecule type: DNA
A/Residues: 1-363 <ROW>
A/Cross-references: UNIPROT:P07266; GB:247047; EMBL:X38061; NID:g603997; PID:g763366; MI
R/Kreike, J.; Schulze, M.; Ahne, F.; Lang, B.F.
EMBO J. 6, 2123-2129, 1987
A/Title: A yeast nuclear gene, MRS1, involved in mitochondrial RNA splicing: nucleotide
A/Reference number: A91075; MUID:88004424; PMID:2443348
A/Accession: A29684
A/Molecule type: DNA
A/Residues: 1-181, 'P', 183-317, 'A', 319-363 <KRE>
A/Cross-references: EMBL:X05509; NID:g3987; PIDN:CAA29053.1; PID:g3988
C/Genetics:
A/Gene: SGD:MRS1; PET157
A/Cross-references: SGD:S0001460; MIPS:YIR021w
A/Map position: 9R
A/Genome: nuclear
C/Keywords: mitochondrion

Query Match          13.8%; Score 68; DB 2; Length 363;
Best Local Similarity 26.0%; Pred. No. 10;
Matches 25; Conservative 21; Mismatches 32; Indels 18; Gaps 4;
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 39.9444 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-25
Perfect score: 494
Sequence: 1 KLEELQKQVSYKGDPIVQH.....LNYQLKIKVICDKSGDVAA 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	494	100.0	163	Q9N145	Q9N145 macaca mula
2	494	100.0	770	1 STA3 BOVIN	P61635 bos taurus
3	494	100.0	770	1 STA3 HUMAN	P40763 homo sapien
4	494	100.0	770	1 STA3 MOUSE	P42227 mus musculus
5	491	99.4	770	1 STA3 RAT	P52631 rattus norv
6	490	99.2	771	2 Q6DV79	Q6dv79 gallus gall
7	489	99.0	769	2 Q9PVX8	Q9pvx8 xenopus lae
8	487	98.6	161	2 Q704W5	Q704w5 bos taurus
9	475	96.2	766	2 Q7ZXX3	Q7zxx3 xenopus lae
10	474	96.0	414	2 Q7ZTS5	Q7zt55 brachydanio
11	474	96.0	786	2 Q6NV46	Q6nv46 brachydanio
12	474	96.0	806	2 Q93599	Q93599 brachydanio
13	472	95.5	765	2 Q6DVU3	Q6dvf3 oryzias lat
14	472	95.5	785	2 Q6GUE7	Q6gue7 oryzias lat
15	461	93.3	764	2 Q90V16	Q90y16 tetraodon f
16	453	91.7	767	2 Q13133	Q13133 oncorhynch
17	315	63.8	751	2 Q8JGNO	Q8jgn0 xenopus lae
18	311	63.0	712	2 Q6P6Q7	Q6p6q7 rattus norv
19	311	63.0	749	2 Q8C497	Q8c497 mus musculus
20	311	63.0	749	2 Q9QXK0	Q9qxx0 rattus norv
21	310	62.8	712	2 Q9QK94	Q9qk94 mus musculus
22	310	62.8	749	2 Q8C3V4	Q8c3v4 mus musculus
23	310	62.8	749	2 Q9D323	Q9d323 mus musculus
24	310	62.8	750	1 STA1 HUMAN	P42224 homo sapien
25	310	62.8	750	2 Q68D00	Q68d00 homo sapien
26	310	62.8	755	2 Q8C8M3	Q8cm3 mus musculus
27	309	62.6	758	2 Q90Y17	Q90y17 tetraodon f
28	304	61.5	757	2 Q764M5	Q764m5 sus scrofa
29	294	59.5	1153	2 Q8JF85	Q8jfs5 brachydanio
30	292	59.1	754	2 Q13131	Q13131 oncorhynch
31	292	59.1	754	2 Q13132	Q13132 oncorhynch

32	291	58.9	748	1 STA4 HUMAN	Q14765 homo sapien
33	290	58.7	718	2 Q801Y2	Q801y2 carassius a
34	288	58.3	528	2 Q8JF08	Q8jfu8 brachydanio
35	285	57.7	737	2 Q90Y15	Q90y15 tetraodon f
36	283	57.3	749	1 STA4 MOUSE	P42228 mus musculus
37	282	57.1	748	2 Q66HB2	Q66hb2 rattus norv
38	280	56.7	553	2 Q8JF07	Q8jfu7 brachydanio
39	280	56.7	651	2 Q7Z253	Q7z253 brachydanio
40	280	56.7	652	2 Q7Z277	Q7z277 brachydanio
41	280	56.7	657	2 Q8AW24	Q8aw24 brachydanio
42	280	56.7	667	2 Q8AW20	Q8aw20 brachydanio
43	279	56.5	749	1 STA1 MOUSE	P42225 mus musculus
44	261	52.8	749	2 Q93598	Q93598 brachydanio
45	261	52.8	749	2 Q6P943	Q6p943 brachydanio

ALIGNMENTS

RESULT 1

Q9N145	PRELIMINARY;	PRT;	163 AA.
AC	Q9N145;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Signal transducer and activator of transcription (Fragment).		
GN	Name=STAT3;		
OS	Macaca mulatta (Rhesus macaque).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;		
OC	Cercopitheciinae; Macaca.		
OX	NCBI_TaxID=9544;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Arredondo J.		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF227560; AAF73401.1; -		
DR	HSSP; P42227; 1BG1.		
DR	GO; GO:0005634; C:nucleus; IEA.		
DR	GO; GO:004871; F:signal transducer activity; IEA.		
DR	GO; GO:0003700; P:transcription factor activity; IEA.		
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.		
DR	GO; GO:007165; P:signal transduction; IEA.		
DR	InterPro; IPR008967; P53 like_DNA_bnd.		
DR	InterPro; IPR001217; STAT.		
DR	Pfam; PF01017; STAT_alpha; 1.		
DR	Pfam; PF02864; STAT_bind; 1.		
FT	NON_TER 1		
FT	NON_TER 163		
SQ	SEQUENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;		

Query Match 100.0%; Score 494; DB 2; Length 163;

Best Local Similarity 100.0%; Pred. No. 1.3e-46; Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQKQVSYKGDPIVQHRLPMLERIVLFLFNLMKSAFVVERQPCMPHDPRLVIKT 60

Db 52 KLEELQKQVSYKGDPIVQHRLPMLERIVLFLFNLMKSAFVVERQPCMPHDPRLVIKT 111

Qy 61 GVQFTTKVRLLVKFPPELVOLKIKVICDKSGDVAA 96

Db 112 GVQFTTKVRLLVKFPPELVOLKIKVICDKSGDVAA 147

RESULT 2

STA3 BOVIN

ID STA3 BOVIN STANDARD; PRT; 770 AA.

AC P61635;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Signal transducer and activator of transcription 3.

GN Name=STAT3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Mammary gland;
 RC Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
 RA "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
 RT during ruminant evolution.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes (By similarity).
 CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation (By similarity).
 CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AJ620655; CAP06182.1; -
 DR PROSITE; PSS0001; SH2; 1.
 KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
 FT Transcription regulation.
 FT DOMAIN 580 670
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT MOD_RES 727 727 Phosphoserine (By similarity).
 SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73EB3274 CRC64;
 Query Match 100.0%; Score 494; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 7.7e-46;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLEELQKYSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPWHPDRPLVIKT 60
 Db 282 KLEELQKYSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPWHPDRPLVIKT 341
 Qy 61 GVQFTTKRLVLKFPPELNYQLKIKVCIDKDSGDVAA 96
 Db 342 GVQFTTKRLVLKFPPELNYQLKIKVCIDKDSGDVAA 377
 RESULT 3
 STA3 HUMAN
 ID STA3 HUMAN STANDARD; PRT; 770 AA.
 AC P40763; O14916; Q9BW54;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 GN Name=STAT3; Synonyms=APRF;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Placenta;
 RC MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
 RX Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,

RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
 RT related transcription factor involved in the gp130-mediated signaling
 RT pathway.";
 RL Cell 77:63-71(1994).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
 RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
 RT "Highly conserved amino-acid sequence between murine STAT3 and a
 RT revised human STAT3 sequence.";
 RL Gene 213:119-124(1998).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
 RP Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Rajkumar N., Yi Q., Nickerson D.A.;
 RT "SeattlesNPs. NHDBI HU6682 program for genomic applications, UW-
 RT FHCR, Seattle, WA URL: <http://pga.gs.washington.edu/>.";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
 RP TISSUE=Kidney, and Pancreas;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 564-704 FROM N.A.
 RP TISSUE=Liver;
 RC Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
 RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN PHOSPHORYLATION ON SERINE.
 RP MEDLINE=95215843; PubMed=7701321;
 RX Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
 RT "Requirement of serine phosphorylation for formation of STAT-promoter
 RT complexes.";
 RL Science 267:1990-1994 (1995).
 RN [7]
 RN INTERACTION WITH NCOAL.
 RP PubMed=11773079; DOI=10.1074/jbc.M11486200;
 RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
 RT "Functional interaction of STAT3 transcription factor with the
 RT coactivator NcoA/SRC1a.";
 RL J. Biol. Chem. 277:8004-8011(2002).
 CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes.
 CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC

CC IsoId=P40763-1; Sequence=Displayed;
CC Names=Del-701;
CC ISOId=P40763-2; Sequence=VSP_010474;
CC TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
CC muscle, kidney and pancreas.
CC -1- PPM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity.
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; L29277; AAS58374.1; -;
CC ENBL; AJ012463; CAA10032.1; -;
CC ENBL; AY572796; AAS66986.1; -;
CC ENBL; BC000627; AAH00627.1; -;
CC ENBL; BC014482; AAH14482.1; -;
CC ENBL; AF029311; AAB84254.1; -;
CC PIR; A54444; A54444.
CC HSSP; P42227; IBL1.
CC TRANSFAC; T01493; -;
CC Genew; HGNC:11364; STAT3.
CC H-InvDB; HIX0013840; -;
CC MIM; 102582; -;
CC GO; GO:0005737; C:cytoplasm; TAS.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . . ; TAS.
CC GO; GO:0003700; F:transcription factor activity; TAS.
CC GO; GO:0006928; P:cell motility; TAS.
CC GO; GO:0007259; P:JAK-STAT cascade; TAS.
CC GO; GO:0001222; P:negative regulation of transcription from P. . . ; TAS.
CC GO; GO:0007399; P:neurogenesis; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR008967; P53 like_DNA_bnd.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001217; STAT.
CC Pfam; PF00017; SH2; 1.
CC Pfam; PF01017; STAT_alpha; 1.
CC Pfam; PF02864; STAT_bind; 1.
CC Pfam; PF02865; STAT_int; 1.
CC PROSITE; PS00001; SH2; 1.
CC KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
CC Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
CC FT DOMAIN 580 670
CC FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
CC FT MOD_RES 727 727 Phosphoserine (By similarity).
CC FT VARSPPLIC 701 701 Missing (in isoform Del-701).
CC FT FTID=VSP_010474.
CC FT VARIANT 32 32 Q -> K (in dbSNP:1803125).
CC FT FTID=VAR_018683.
CC FT VARIANT 143 143 M -> I.
CC FT FTID=VAR_018679.
CC FT CONFLICT 288 288 Q -> H (in Ref. 1).
CC FT CONFLICT 460 460 P -> S (in Ref. 1).
CC FT CONFLICT 548 548 K -> N (in Ref. 1).
CC FT CONFLICT 561 561 F -> Y (in Ref. 1).
CC FT CONFLICT 667 667 V -> L (in Ref. 1).
CC FT CONFLICT 730 730 T -> A (in Ref. 1).
CC SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
Query Match 100.0%; Score 494; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 7.7e-46;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQKQVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60

Db 282 KKLEELQKQVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVQFTTKVRLLVKFPPELNYQKIKVCIDKDSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQKIKVCIDKDSGDVAA 377
RESULT 4
STAT3 MOUSE
ID STAT3_MOUSE STANDARD; PRT; 770 AA.
AC P42227;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=Stat3; Synonyms=Aprf;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
RP AND 632-640.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RL Cell 77:63-71(1994).
[2]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Thymus;
RX MEDLINE=94188718; PubMed=8140422;
RA Zhong Z., Wen Z., Darnell J.E. Jr.;
RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
RT response to epidermal growth factor and interleukin-6.";
RL Science 264:95-98(1994).
[3]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Brain;
RX MEDLINE=95014185; PubMed=7523373;
RA Raz R., Durbin J.E., Levy D.E.;
RT "Acute phase response factor and additional members of the interferon-
RT stimulated gene factor 3 family integrate diverse signals from
RT cytokines, interferons, and growth factors.";
RL J. Biol. Chem. 269:24391-24395(1994).
[4]
RN SEQUENCE FROM N.A. (ISOFORM STAT3B).
RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
RX MEDLINE=96016116; PubMed=7568080;
RA Schaefer T.S., Sanders L.K., Nathans D.;
RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
RT form of Stat3.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
[5]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=129/SVJ;
RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
RA Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zon L., Oka T.,
RA Dewar K., Hennighausen L.;
RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
RT zebrafish to mouse.";
RL Genomics 71:150-155(2001).
[6]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=C57BL/6J, and NOD/LtJ;
RA Davoodi-Semirami A., She J.-X.;
RT "A mutant Stat3b with weaker DNA binding defines a key defective
RT pathway in non-obese diabetic (NOD) mice.";

Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

[7]
SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Butterfield Y.S.N., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Smailus D.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS
RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
RA Wen Z., Zhong Z., Darnell J.E. Jr.;
RT "Maximal activation of transcription by Stat1 and Stat3 requires both
tyrosine and serine phosphorylation.";
Cell 82:241-250(1995).
[9]
X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
RA Becker S., Groner B., Mueller C.W.;
RT "Three-dimensional structure of the Stat3beta homodimer bound to
DNA.";
Nature 394:145-151(1998).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
acute-phase protein genes. STAT3B interacts with the N-terminal
part of JUN to activate such promoters in a cooperative way.
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
member (at least STAT1). Interacts with NCOAL (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
in response to phosphorylation.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=Stat3A;
IsoId=P42227-1; Sequence=Displayed;
Name=Stat3B;
IsoId=P42227-2; Sequence=VSP_006287;
Name=Del-701;
IsoId=P42227-3; Sequence=VSP_010475;
CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
kidney. STAT3B is also detected in the liver, although in a much
less abundant manner.
CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
is important for the formation of stable DNA-binding STAT3
homodimers and maximal transcriptional activity (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.

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entities requires a license agreement (see <http://www.ebi.ac.uk/announcements>
or send an email to license@ebi.ac.uk).

CC DR EMBL; L29278; AAA37254.1; -
DR EMBL; U06922; AAA19452.1; -
DR EMBL; U08378; AAA56668.1; -
DR EMBL; U30709; AAC52612.1; -
DR EMBL; AE246978; AAL59017.1; -
DR EMBL; AY299489; AAG75418.1; -
DR EMBL; AY299490; AAG75419.1; -
DR EMBL; BC003806; AAH03806.1; -
DR PIR; I49508; I49508
DR PDB; 1BGL; X-ray; A=1-722.
DR TRANSFAC; T01574; -
DR MGD; MGI:103038; Stat3.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005677; F:DNA binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016563; F:transcriptional activator activity; IDA.
DR GO; GO:0007259; P:JAK-STAT cascade; IDA.
DR GO; GO:0006357; P:regulation of transcription from Pol II promoter; IDA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR00980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PSS0001; SH2; 1.
KW 3D-structure; Activator; Acute phase; Alternative splicing;
KW Direct protein sequencing; DNA-binding; Nuclear protein;
KW Phosphorylation; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine.
FT VARSPPLIC 716 770 TTCSNTIDLPMSRTLDLSLMQFGNGEGAPSPAGGQPESLT
FT FT FIDAVWK (in isoform
FT FT Stat3B).
FT FT /FTId=VSP_006287.
FT FT Missing (in isoform Del-701).
FT FT /FTId=VSP_010475.
FT FT S->A: Decreased transcriptional
activation.
FT FT E -> K (in Ref. 2).
FT FT S -> T (in Ref. 2 and 4).
FT FT M -> I (in Ref. 1).

Query Match	100.0%;	Score 494;	DB 1;	Length 770;
Best Local Similarity	100.0%;	Pred. No. 7.7e-46;		
Matches	96;	Conservative	0;	Mismatches 0; Gaps 0;

Qy 1 KCLLELOQKVSXKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHPDRPLVIKT 60
DB 282 KCLLELOQKVSXKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHPDRPLVIKT 341

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Qy 61 GVOFTTKVRLVLPPELNYQLKIKVCIDKDSGDVAA 96
Db 342 GVOFTTKVRLVLPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 5
STA3 RAT STANDARD; PRT; 770 AA.
ID STA3 RAT
AC PS2631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=Stat3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
RA Ripberger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
RA Fey G.H.;
RT "Transcription factors Stat3 and Stat5b are present in rat liver
RT nuclei late in an acute phase response and bind interleukin-6 response
RT elements."
RL J. Biol. Chem. 270:29998-30006(1995).
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation (By similarity).
CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC -----
DR EMBL; X91810; CAA62920.1; -.
DR HSSP; P42227; 1BG1.
DR RGD; 3772; Stat3.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
DR Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 88039 MW; D74A0C76954754ED CRC64;

Query Match 99.4%; Score 491; DB 1; Length 770;
Best Local Similarity 99.0%; Pred. No. 1.7e-45;
Matches 95; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVFKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVDLFRLMKSAFVVERQPCMPHDPRLVFKT 341

RESULT 6
Q6DV79 PRELIMINARY; PRT; 771 AA.
ID Q6DV79
AC Q6DV79;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Signal transducer and activator of transcription 3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV641397; AAT64887.1; -.
DR GO; GO:0005634; Cnucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
DR SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match 99.2%; Score 490; DB 2; Length 771;
Best Local Similarity 99.0%; Pred. No. 2.1e-45;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVFKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVFKT 341

RESULT 7
Q9PVX8 PRELIMINARY; PRT; 769 AA.
ID Q9PVX8
AC Q9PVX8;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Stat 3.
GN Name=stat 3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;

Query Match 99.4%; Score 491; DB 1; Length 770;
Best Local Similarity 99.0%; Pred. No. 1.7e-45;
Matches 95; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RA Nishinakamura R., Mateumoto Y., Matsuda T., Ariizumi T., Heike T.,
 RA Aashima M., Yokota T.;
 RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
 RT embryos independent of BMP-4.";
 RL Dev. Biol. 216:481-490(1999).
 RL EMBL; AB017701; BAA86061.1; -.
 DR HSSP; P42227; 1BG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS0001; SH2; 1.
 DR SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;
 Query Match 99.0%; Score 489; DB 2; Length 769;
 Best Local Similarity 99.0%; Pred. No. 2.8e-45;
 Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KKLLELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQCPMPHDPRLVIKT 60
 DB 282 KKLLELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQCPMPHDPRLVIKT 341
 QY 61 GVOFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 96
 DB 342 GVOFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 377
 RESULT 8
 Q704W5 PRELIMINARY; PRT; 161 AA.
 ID Q704W5
 AC Q704W5
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Signal transducer and activator of transcription 3 (Fragment).
 GN Name=stat3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Mollenaar A., Wheeler T.T., McCracken J.Y., Seyfert H.M.;
 RT "The STAT3-encoding gene resides within the 40 kbp gap between the
 RT STAT5A- and STAT5B-encoding gene in cattle.";
 RL Anim. Genet. 31:333-334(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AJ620661; CAFO6188.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 FT NON_TER

FT NON_TER 161
 SQ SEQUENCE 161 AA; 18342 MW; 5DCE8F2C3A48191 CRC64;
 Query Match 98.6%; Score 487; DB 2; Length 161;
 Best Local Similarity 99.0%; Pred. No. 7.7e-46;
 Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KKLLELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQCPMPHDPRLVIKT 60
 DB 16 KKLLELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQCPMPHDPRLVIKT 75
 QY 61 GVOFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 96
 DB 76 GVOFTTKVRLVLPPELNYQLKIKVCIDKSGDVAA 111
 RESULT 9
 Q7ZAK3 PRELIMINARY; PRT; 766 AA.
 ID Q7ZAK3
 AC Q7ZAK3
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Stat3-A protein.
 GN Name=stat3-A;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=223411132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC044717; AAH44717.1; -.
 DR HSSP; P42227; 1BG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007165; F:transcription factor activity; IEA.

DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR008967; P33_like_DNA_bnd.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001217; STAT.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF01017; STAT alpha; 1.
DR Pfam: PF02864; STAT_bind; 1.
DR Pfam: PF02865; STAT_int; 1.
DR SMART; SMO0252; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
SQ SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;

Query Match 96.2%; Score 475; DB 2; Length 766;
Best Local Similarity 95.8%; Pred. No. 9.7e-44;
Matches 92; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KKLLELOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 282 KKLLELOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 341

Qy 61 GVQFTTKVRLVKFPPELNYQLKIKVCIDKSGDVAA 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 342 GVQFTTKVRLVKFPPELNYQLKIKVCIDKSGEGAA 377

RESULT 10
Q7ZTS5 PRELIMINARY; PRT; 414 AA.
AC Q7ZTS5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC045276; AAH45276.1; -.
DR HSSP; P42227; IBL1.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:000526-68; stat3.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.

DR GO: GO:0004871; F:signal transducer activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR008967; P53_like_DNA_bnd.
DR InterPro: IPR001217; STAT.
DR Pfam: PF01017; STAT alpha; 1.
DR Pfam: PF02864; STAT_bind; 1.
DR Pfam: PF02865; STAT_int; 1.
SQ SEQUENCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;

Query Match 96.0%; Score 474; DB 2; Length 414;
Best Local Similarity 93.8%; Pred. No. 6.2e-44;
Matches 90; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKLLELOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 283 KKLLELOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 342

Qy 61 GVQFTTKVRLVKFPPELNYQLKIKVCIDKSGDVAA 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 343 GVQFTTKVRLVKFPPELNYQLKIKVCIDKSGDVAA 378

RESULT 11
Q6NV46 PRELIMINARY; PRT; 786 AA.
AC Q6NV46;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC068320; AAH68320.1; -.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0004871; F:signal transducer activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.

DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR	InterPro; IPR008967; P53_like_DNA_bnd.	
DR	InterPro; IPR000980; SH2.	
DR	InterPro; IPR001217; STAT.	
DR	Pfam; PF00017; SH2; 1.	
DR	Pfam; PF01017; STAT_alpha; 1.	
DR	Pfam; PF02864; STAT_bind; 1.	
DR	Pfam; PF02865; STAT_int; 1.	
DR	PROSITE; PS00001; SH2; 1.	
SQ	SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;	
	Query Match 96.0%; Score 474; DB 2; Length 786;	
	Best Local Similarity 93.8%; Pred. No. 1.3e-43;	
	Matches 90; Conservative 5; Mismatches 1; Indels 0; Gaps 0	
Qy	1 KKEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPDRPLVIKT 60	
Db	283 KKEELQOKVSYKGDPIIQRHPALAEKIVDLFRNLKMSAFVVERQPCMPMHDPDRPLVIKT 342	
	: : : : : : : : : :	
Qy	61 GVQFTTKVRLLVKFPPELVNYQLKIKVICDKDSGDVAA 96	
Db	343 GVQFTTKVRLLVKFPPELVNYQLKIKVICDKESGDVAA 378	
	: : : : : : : : :	
RESULT 12		
ID	O93599 PRELIMINARY; PRT; 806 AA.	
AC	O93599;	
DT	01-NOV-1998 (TReMBLrel. 08, Created)	
DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)	
DT	01-MAR-2004 (TReMBLrel. 26, Last annotation update)	
DE	Transcription factor.	
GN	Name=stat3;	
OS	Brachydanio rerio (Zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OC	NCBI_TaxID=7955;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Oates A.C.;	
RL	Thesis (1998), University of Melbourne, Australia.	
DR	EMBL; AJ005693; CAA06677.1; -.	
DR	HSSP; P4227; 1BG1.	
DR	ZFIN; ZDB-GENE-980526-68; stat3.	
DR	GO; GO:0005634; C:nucleus; IEA.	
DR	GO; GO:0004871; F:signal transducer activity; IEA.	
DR	GO; GO:0003700; F:transcription factor activity; IEA.	
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.	
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR	InterPro; IPR008967; P53_like_DNA_bnd.	
DR	InterPro; IPR000980; SH2	
DR	InterPro; IPR001217; STAT.	
DR	Pfam; PF00017; SH2; 1.	
DR	Pfam; PF01017; STAT_alpha; 1.	
DR	Pfam; PF02864; STAT_bind; 1.	
DR	Pfam; PF02865; STAT_int; 1.	
DR	SMART; SM00252; SH2; 1.	
DR	PROSITE; PS00001; SH2; 1.	
SQ	SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3942 CRC64;	
	Query Match 96.0%; Score 474; DB 2; Length 806;	
	Best Local Similarity 93.8%; Pred. No. 1.3e-43;	
	Matches 90; Conservative 5; Mismatches 1; Indels 0; Gaps 0	
Qy	1 KKEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPDRPLVIKT 60	
Db	283 KKEELQOKVSYKGDPIIQRHPALAEKIVDLFRNLKMSAFVVERQPCMPMHDPDRPLVIKT 342	
	: : : : : : : : :	
Qy	61 GVQFTTKVRLLVKFPPELVNYQLKIKVICDKDSGDVAA 96	
Db	343 GVQFTTKVRLLVKFPPELVNYQLKIKVICDKESGDVAA 378	
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DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;

Query Match          95.5%; Score 472; DB 2; Length 785;
Best Local Similarity 93.8%; Pred. No. 2.2e-43;
Matches 90; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 283 KLEELQOKVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPMHPDRPLVIKT 342
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
Db 343 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKESGDVAA 378

RESULT 15
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
SEQUENCE FROM N.A.
RP Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FPE18BEFD8BE CRC64;

Query Match          93.3%; Score 461; DB 2; Length 764;
Best Local Similarity 91.7%; Pred. No. 3.5e-42;
Matches 88; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 283 KLEELQOKVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPMHPDRPLVIKT 342
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
Db 343 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKESGDVAA 378
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Search completed: May 25, 2005, 17:43:42
Job time : 40.9444 secs

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OM protein - protein search, using sw model
Run on: May 25, 2005, 17:14:45 ; Search time 121.891 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-29
Perfect score: 1169
Sequence: 1 NHPTAAVTEKQMLEQHLQ.....IKTGQFATAVALLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003Bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1160	99.2	229	AAy72860	Aay72860 Mouse Sta
2	1155	98.8	229	AAy72850	Aay72850 Mouse Sta
3	1155	98.8	252	AAy72846	Aay72846 Mouse Sta
4	1155	98.8	271	AAy72841	Aay72841 Mouse Sta
5	1155	98.8	770	AAy72082	Aay72082 Mouse Sta
6	1155	98.8	770	AAW03176	AAW03176 Mouse Sta
7	1151	98.5	229	AAy72863	AAy72863 Mouse Sta
8	1150	98.4	229	AAy72862	AAy72862 Mouse Sta
9	1144	97.9	720	AAe22055	AAe22055 Human Sta
10	1144	97.9	769	ABBS7164	ABBS7164 Mouse isc
11	1144	97.9	769	AAE22054	AAE22054 Human Sta
12	1144	97.9	769	AAE22056	AAE22056 Human pro
13	1144	97.9	770	AAE22095	AAE22095 Mouse liv
14	1144	97.9	770	AAy03768	AAy03768 Human STA
15	1144	97.9	770	AAAB12377	AAAB12377 N-termina
16	1144	97.9	770	AAE14652	AAE14652 Murine ST
17	1144	97.9	770	ABG69497	ABG69497 Human bai
18	1144	97.9	770	ABU10476	ABU10476 Mouse STA
19	1144	97.9	770	ADN04365	ADN04365 Antipsori
20	1144	97.9	770	ADP54789	ADP54789 Human PRO
21	1144	97.9	793	AAAB58442	AAAB58442 Lung canc
22	1141	97.6	770	ADDA4738	ADDA4738 Rat Prote
23	1140.5	97.6	228	AAy72861	AAy72861 Mouse Sta
24	1139	97.4	770	AAAB2993	AAAB2993 Human pia
25	1139	97.4	770	AAAB19964	AAAB19964 Human sig

ALIGNMENTS

RESULT 1

AAy72860
ID AAY72860 standard; protein; 229 AA.

AC AAY72860;

DT 31-MAY-2001 (first entry)

DE Mouse Stat3 mutant (L148A,V151A,T346A,K348A,R350A) protein fragment.

KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
cellular transformation; dysproliferative disease; cancer; psoriasis;
therapy; mutant; mutein.

OS Mus musculus.

FH Key Location/Qualifiers
FT Region 1..25

FT /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"

FT Misc-difference 19

FT /note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein"

FT Misc-difference 22

FT /note= "Wild type Val substituted with Ala corresponds to 151 position of Stat-3 protein"

FT Region 213..229

FT /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"

FT Misc-difference 217

FT /note= "Wild type Thr substituted with Ala corresponds to 346 position of Stat-3 protein"

FT Misc-difference 219

FT /note= "Wild type Lys substituted with Ala corresponds to 348 position of Stat-3 protein"

FT Misc-difference 221

FT /note= "Wild type Arg substituted with Ala corresponds to 350 position of Stat-3 protein"

PN WO200116605-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023822.

XX 31-AUG-1999; 99US-00387418.

XX (UYRQ) UNIV ROCKEFELLER.

XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JB;
PI WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX Example 4; Page; 86pp; English.
XX The present sequence is mouse Stat3 mutant protein fragment containing
CC 130-358 amino acids of Stat3 protein. This mutant is obtained by
CC replacing Leu 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Lys 348
CC with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates
CC to methods for identifying interacting regions of transcription factors
CC and methods for identifying agents which modulates the interaction
CC between a transcription factor such as c-Jun and a Stat protein such as
CC Stat-1 and Stat-3, useful for modulating gene transcription e.g.,
CC cellular transformation. These identifying agents are used in the
CC treatment of dysproliferative diseases and also for treating cancer and
CC psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil
CC domain, DNA binding domain, linker domain, SH2 domain and transactivation
CC domain
XX SQ Sequence 229 AA;
Query Match 99.2%; Score 1160; DB 4; Length 229;
Best Local Similarity 99.1%; Pred. No. 1.5e-98;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 1 NHPTAAVVTKEQMLQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Qy 61 GNNQSVTRQKMQQLQMLTALDQMRRSIVSELQKLVLSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQKMQQLQMLTALDQMRRSIVSELQKLVLSAMEYVQKTLTDEELADWKRPEI 120
Qy 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIKLELQKLVSKYKGDPIVQHRPMLERI 180
Db 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIKLELQKLVSKYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
RESULT 2
AA72850
ID AAY72850 standard; protein; 229 AA.
XX AAY72850;
AC AAY72850;
XX 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #8 (130-358 amino acids).
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX Mus musculus.
XX Key Location/Qualifiers
FH Region 1. .25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
FT Region 213. .229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
PN
XX

PD 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JB;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX Claim 65; Page 76-77; 86pp; English.
XX The present sequence is mouse Stat3 protein fragment containing 130-358
CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
CC to c-Jun protein in the cell extract. The invention relates to methods
CC for identifying interacting regions of transcription factors and methods
CC for identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX SQ Sequence 229 AA;
Query Match 98.8%; Score 1155; DB 4; Length 229;
Best Local Similarity 98.7%; Pred. No. 4.4e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 1 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Qy 61 GNNQSVTRQKMQQLQMLTALDQMRRSIVSELQKLVLSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQKMQQLQMLTALDQMRRSIVSELQKLVLSAMEYVQKTLTDEELADWKRPEI 120
Qy 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIKLELQKLVSKYKGDPIVQHRPMLERI 180
Db 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIKLELQKLVSKYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
RESULT 3
AA72846
ID AAY72846 standard; protein; 252 AA.
XX AAY72846;
XX 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #4 (107-358 amino acids).
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX Mus musculus.
XX Key Location/Qualifiers
FH Region 24. .48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
FT Region 236. .252
FT

KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX

OS Mus sp.
 XX WO9508629-A1.
 XX 30-MAR-1995.
 XX 26-SEP-1994; 94WO-US010849.
 XX 24-SEP-1993; 93US-00126588.
 XX 24-SEP-1993; 93US-00126595.
 XX 11-MAR-1994; 94US-00212184.
 XX 11-MAR-1994; 94US-00212185.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 XX WPI; 1995-139598/18.
 XX N-PSDB; AAQ89340.

Receptor recognition factor implicated in transcriptional stimulation of
 genes - useful in drug screening assays and/or for treating cellular
 debilitations, derangements and/or dysfunctions, etc.

Claim 1; Page 107-110; 160pp; English.

XX A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX

SQ Sequence 770 AA;

Query Match 98.8%; Score 1155; DB 2; Length 770;
 Best Local Similarity 98.7%; Pred. No. 2.2e-97;
 Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
 DB 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
 QY 61 GNNQSVTRQMKQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 120
 DB 190 GNNQSVTRQMKQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 249
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLERI 180
 DB 250 ACIGGPPNICLDRLNWIITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALIVKFPPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALIVKFPPEL 358

RESULT 6
 AA03176
 ID AA03176 standard; protein; 770 AA.
 XX

XX AA03176;
 XX AC
 XX 24-OCT-1996 (first entry)
 XX DE Mouse STAT4.
 XX

KW STAT; STAT4; signal transducer and activator of transcription;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW autoimmune disease; antagonist; therapy.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 XX 398. .508
 XX Domain /label= DNA_binding_domain
 XX /note= "Claim 3, page 110"

XX WO9620954-A2.
 XX 11-JUL-1996.
 XX 28-DEC-1995; 95WO-US017025.
 XX 06-JAN-1995; 95US-00369796.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Darnell JE, Wen Z, Horvath CM, Zhong Z;
 XX WPI; 1996-333941/33.
 XX N-PSDB; AAT31280.

XX New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
 PT preventing or treating cellular dysfunction, e.g. oncogenesis,
 PT inflammation, parasitic disease or autoimmunity.
 XX

XX Disclosure; Page 87-90; 138pp; English.

XX Mouse signal transducer and activator of transcription (STAT) protein
 CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
 CC ligand-activated receptor kinase complexes followed by nuclear
 CC translocation and DNA binding to activate transcription. Recombinant
 CC STAT4 can be obt'd. using cDNA clone 19sf6 (AAT31278) obt'd. from
 CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
 CC AA03167) capable of both receptor recognition and message delivery via
 CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
 CC DNA binding domains (see also AA03165-75) are useful for screening
 CC antagonists used to inhibit STAT-mediated signal transduction and
 CC activation of transcription

XX Sequence 770 AA;

Query Match 98.8%; Score 1155; DB 2; Length 770;
 Best Local Similarity 98.7%; Pred. No. 2.2e-97;
 Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
 DB 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
 QY 61 GNNQSVTRQMKQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 120
 DB 190 GNNQSVTRQMKQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 249
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLERI 180
 DB 250 ACIGGPPNICLDRLNWIITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALIVKFPPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALIVKFPPEL 358

RESULT 7
 AA72863
 ID AA72863 standard; protein; 229 AA.

XX AA72863;
 XX AC
 XX AA72863;

DT 31-MAY-2001 (first entry)
 DE Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutin.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Misc-difference 22
 FT /note= "Wild type Val substituted with Ala corresponds to
 FT 151 position of Stat-3 protein"
 FT Region 213. .229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 DR
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 PT
 XX Claim 66; Page 86; 86pp; English.
 PS
 XX The present sequence is mouse Stat3 mutant (V151A) protein fragment
 CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
 CC by replacing Val 151 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;
 Query Match 98.5%; Score 1151; DB 4; Length 229;
 Best Local Similarity 98.3%; Pred. No. 1e-97;
 Matches 225; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHLQDVRRKRVODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 1 NHPTAAVVTKEQOMLEQHLQDARRKRVODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 QY 61 GNNQSVTRQMKQMLEQMLTALDQRRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 120
 DB 61 GNNQSVTRQMKQMLEQMLTALDQRRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 120
 QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
 QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVIKTVQFATAVALLVKPPEL 229
 DB 181 VELFRNLMSAFVVERQPCMPHPDRPLVIKTVQFATAVALLVKPPEL 229

RESULT 8
 AAY72862
 ID AAY72862 standard; protein; 229 AA.
 XX
 AC AAY72862;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutin.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Misc-difference 19
 FT /note= "Wild type Leu substituted with Ala; corresponds
 FT to 148 position of Stat-3 protein"
 FT Region 213. .229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 DR
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 PT
 XX Claim 66; Page 85; 86pp; English.
 PS
 XX The present sequence is mouse Stat3 mutant (L148A) protein fragment
 CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
 CC by replacing Leu 148 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;
 Query Match 98.4%; Score 1150; DB 4; Length 229;
 Best Local Similarity 98.3%; Pred. No. 1.3e-97;
 Matches 225; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHLQDVRRKRVODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 1 NHPTAAVVTKEQOMLEQHLQDVRRKRVODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 QY 61 GNNQSVTRQMKQMLEQMLTALDQRRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 120
 DB 61 GNNQSVTRQMKQMLEQMLTALDQRRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 120

QY 121 ACIGPPNICLDRLNWTSLAESOLQTRQOIKKLEELQKQSVKGDPIVQHRPMLERI 180
 |||||
 Db 121 ACIGPPNICLDRLNWTSLAESOLQTRQOIKKLEELQKQSVKGDPIVQHRPMLERI 180
 |||||
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVITKGVQFATAVALLVKFPPEL 229
 |||||
 Db 181 VELFRNLKSAFVVERQPCMPHDPRLVITKGVQFATAVALLVKFPPEL 229
 |||||

RESULT 9

AAE22055
 ID AAE22055 standard; protein; 720 AA.

AC AAE22055;

DT 25-JUL-2002 (first entry)

XX Human Stat3beta protein.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 713..714
 FT /note= "Encoded by ACA CCA TTC"

PN WO200220032-A1.

XX 14-MAR-2002.

XX 10-SEP-2001; 2001WO-US028254.

XX 08-SEP-2000; 2000US-0231212P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Yu H, Pardoll D, Jove R, Dalton W;

XX WPI; 2002-362218/39.

XX N-PSDB; AAD35066.

XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.

XX Disclosure; Page 87-89; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy

CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC Stat3beta protein
 XX

XX SQ Sequence 720 AA;

Query Match 97.9%; Score 1144; DB 5; Length 720;

Best Local Similarity 97.8%; Pred. No. 2e-96;

Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSQDMDLN 60

Db 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSQDMDLN 189

QY 61 GNNQSVTRQKMQOQLQMLTALDQMRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEI 120

Db 190 GNNQSVTRQKMQOQLQMLTALDQMRRSIVSELAGLLSMEYVQKTLTDEELADWKRQOI 249

QY 121 ACIGPPNICLDRLNWTSLAESOLQTRQOIKKLEELQKQSVKGDPIVQHRPMLERI 180

Db 250 ACIGPPNICLDRLNWTSLAESOLQTRQOIKKLEELQKQSVKGDPIVQHRPMLERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVITKGVQFATAVALLVKFPPEL 229

Db 310 VELFRNLKSAFVVERQPCMPHDPRLVITKGVQFATAVALLVKFPPEL 358

RESULT 10

ABBS57164

ID ABB57164 standard; protein; 769 AA.

AC ABB57164;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related protein sequence SEQ ID NO:398.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX Mus musculus.

XX WO200188188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP004192.

XX 18-MAY-2000; 2000JP-00145977.

XX (UYNI-) UNIV NIHOON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

XX N-PSDB; ABI99454.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by

PT determining the expression profile of a gene group comprising these
 PT genes.

Claim 2; Page 1084-1087; 2690pp; English.

CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (1) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (1). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI999202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention

XX Sequence 769 AA;

Query Match 97.9%; Score 1144; DB 5; Length 769;
 Best Local Similarity 97.8%; Pred. No. 2.2e-96;
 Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQMKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDDFNYKTLKSGQDMQDLN 120
 DB 190 GNNQSVTRQMKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDDFNYKTLKSGQDMQDLN 249
 QY 121 ACIGGPNICLDRLENWITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 180
 DB 250 ACIGGPNICLDRLENWITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 358

RESULT 11

ID AAE22054

XX AAE22054 standard; protein; 769 AA.

AC AAE22054;

DT 25-JUL-2002 (first entry)

XX Human Stat3 protein.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

XX Homo sapiens.

OS WC0200220032-A1.

PN 14-MAR-2002.

PD 10-SEP-2001; 2001WO-US028254.

XX

PR 08-SEP-2000; 2000US-0231212P.

XX

PA (UYJO) UNIV JOHNS HOPKINS.

PA

PA (UYSF-) UNIV SOUTH FLORIDA.

XX

PI Yu H, Pardoll D, Jove R, Dalton W;

XX

XX WPI; 2002-362218/39.

DR

DR N-PSDB; AAD35065.

XX

PT Modulating angiogenesis and an immune response in an individual, for

PT

PT treating a hypoxic or ischemic condition, comprises administering a

PT

PT compound that modulates the activity of a signal transducer and activator

PT

PT of transcription 3.

XX

XX Disclosure; Page 83-85; 94pp; English.

XX

CC The invention relates to a method of modulating angiogenesis and immune

CC

CC response. Method involves administering to an individual a compound that

CC

CC modulate the activity of signal transducer and activator of transcription

CC

CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing

CC

CC hypoxic or ischaemic condition or disorder which is the result of stroke,

CC

CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,

CC

CC tissue ischaemia in the lower extremities, infarction, trauma, vascular

CC

CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,

CC

CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,

CC

CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,

CC

CC mixed connective tissue disease, primary biliary cirrhosis, pernicious

CC

CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,

CC

CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,

CC

CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's

CC

CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune

CC

CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and

CC

CC dense deposit disease. The method is useful in preventing or treating

CC

CC specific proliferative and oncogenic disease which includes sarcomas and

CC

CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,

CC

CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,

CC

CC hypoproliferative disorders, physical trauma, lesions and wounds. The

CC

CC method is also used in gene therapy. The present sequence is human Stat3

CC

XX

XX Sequence 769 AA;

Query Match 97.9%; Score 1144; DB 5; Length 769;
 Best Local Similarity 97.8%; Pred. No. 2.2e-96;
 Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQMKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDDFNYKTLKSGQDMQDLN 120
 DB 190 GNNQSVTRQMKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDDFNYKTLKSGQDMQDLN 249
 QY 121 ACIGGPNICLDRLENWITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 180
 DB 250 ACIGGPNICLDRLENWITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 358

RESULT 12

AAE22056

ID AAE22056 standard; protein; 769 AA.

XX AC AAE22056;
 XX KW Human protein related to angiogenesis regulation.
 XX DT 25-JUL-2002 (first entry)
 XX DE
 XX KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW Sjogren's syndrome; proliferative angiopathy; autoimmune thyroiditis;
 KW nitrogen necrosis; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 XX OS Homo sapiens.
 XX KW WO200220032-A1.
 XX PN 14-MAR-2002.
 XX FD 10-SEP-2001; 2001WO-US028254.
 XX PF 08-SEP-2000; 2000US-0231212P.
 XX PR (UJJO) UNIV JOHNS HOPKINS.
 XX PA (UYSF-) UNIV SOUTH FLORIDA.
 XX KW Yu H, Pardoll D, Jove R, Dalton W;
 XX WPI; 2002-362218/39.
 XX DR
 XX PT Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX FS Disclosure; Page 83-85; 94pp; English.
 XX CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation

SQ Sequence 769 AA;
 Query Match 97.9%; Score 1144; DB 5; Length 769;
 Best Local Similarity 97.8%; Pred. No. 2.2e-96;
 Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEHQLQDVKRVRVODLEQKMKVVENLQDDPFDNYKTLKSGDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEHQLQDVKRVRVODLEQKMKVVENLQDDPFDNYKTLKSGDMQDLN 189
 QY 61 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 190 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI 249
 QY 121 ACIGGPPNICLDRENNWITSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 180
 DB 250 ACIGGPPNICLDRENNWITSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGVQFATAVALVKKPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPMPDRPLVKTGVQFATAVALVKKPEL 358
 RESULT 13
 AAR82995
 ID AAR82995 standard; protein; 770 AA.
 XX AC AAR82995;
 XX DT 25-MAR-1996 (first entry)
 XX DE Mouse liver acute phase response factor.
 XX KW Mouse; acute phase response factor; transcription factor; interleukin-6;
 KW signal transduction; liver; antibody; antisease; ribozyme;
 KW antiinflammatory; antitumor; hypotensive; therapy.
 XX OS Mus musculus.
 XX PN EP676469-A2.
 XX PD 11-OCT-1995.
 XX PF 29-MAR-1995; 9SEP-00104670.
 XX PR 04-APR-1994; 94JP-00065825.
 XX PA (KISH/) KISHIMOTO T.
 XX PI Akira S, Kishimoto T;
 XX WPI; 1995-346089/45.
 XX N-PSDB; AAT05619.
 XX PT New acute phase response factor - for developing inhibitory agents for
 PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
 PT diseases.
 XX PS Claim 10; Page 20-22; 31pp; English.
 XX CC The sequence represents a mouse acute phase response factor (APRF), a
 CC transcription factor related to signal transduction of interleukin-6 (IL-
 CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
 CC library using a polymerase chain reaction product (amplified using
 CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
 CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
 CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
 CC inflammatory disease, leukemia, cancer, osteoclastia, pulmonary
 CC hypertension, etc
 XX SQ Sequence 770 AA;
 Query Match 97.9%; Score 1144; DB 2; Length 770;

Best Local Similarity 97.8%; Pred. No. 2.2e-96;		Best Local Similarity 97.8%; Pred. No. 2.2e-96;	
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;		Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
QY	1 NHPTAAVVTKEQOMLEQHLQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60	Db	130 NHPTAAVVTKEQOMLEQHLQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
Db	130 NHPTAAVVTKEQOMLEQHLQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189	QY	61 GNNQSVTRQKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
QY	61 GNNQSVTRQKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120	Db	190 GNNQSVTRQKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI 249
Db	190 GNNQSVTRQKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI 249	QY	121 ACIGGPPNICLDRLNWIITSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLBERRI 180
QY	121 ACIGGPPNICLDRLNWIITSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLBERRI 180	Db	250 ACIGGPPNICLDRLNWIITSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLBERRI 309
Db	250 ACIGGPPNICLDRLNWIITSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLBERRI 309	QY	181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPPEL 229
QY	181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPPEL 229	Db	310 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPPEL 358
Db	310 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPPEL 358	RESULT 15	
AAAY03768		AAB12377	
ID	AAAY03768 standard; protein; 770 AA.	ID	AAB12377 standard; peptide; 770 AA.
AC	AAAY03768;	AC	AAB12377;
DT	11-JUN-1999 (first entry)	DT	08-NOV-2000 (first entry)
DE	Human STAT3 allelic variant.	DE	N-terminal domain of murine STAT-3 protein.
KW	Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;	KW	STAT; signal transducer and activator of transcription; crystal;
KW	intracellular transcription factor; interleukin-6; medicament; variant;	KW	drug design; murine.
KW	pharmaceutical; autoimmune disease; inflammatory; human.	OS	Mus sp.
OS	Homo sapiens.	Key	Location/Qualifiers
PN	EP905234-A2.	FT Region	4..9 /label= Alpha helix 1
PD	31-MAR-1999.	FT Region	12..21 /label= Alpha helix 2
PF	18-FEB-1998; 98EP-00102774.	FT Region	19..21 /label= 3(10) helix of alpha helix 2
PR	16-SEP-1997; 97EP-00116061.	FT Region	28..33 /label= Alpha helix 3
PA	(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.	FT Region	35..40 /label= Alpha helix 4
PI	Serlupi-Crescenzi O, Della Pietra L;	FT Region	43..47 /label= Alpha helix 5
DR	WPI; 1999-192664/17.	FT Region	50..73 /label= Alpha helix 6
DR	N-PSDB; AAX29281.	FT Region	77..96 /label= Alpha helix 7
XX	New human Signal Transducer and Activator of Transcription 3 (STAT3)	FT Region	99..119 /label= Alpha helix 8
PT	allelic variant useful for treatment of autoimmune and inflammatory	PN	US6087478-A.
PT	disease.	PD	11-JUL-2000.
XX	Claim 2; Page 9-13; 32pp; English.	XX	US6087478-A.
XX	The present sequence represents a predominant allelic variant of human	XX	23-JAN-1998; 98US-00012710.
CC	Signal Transducer and Activator of Transcription 3 (STAT3) protein, an	XX	23-JAN-1998; 98US-00012710.
CC	intracellular transcription factor which mediates IL-6 signals. The	PA	(UYRQ) UNIV ROCKEFELLER.
CC	encoding sequence differs from the original published human STAT3 gene	PI	Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
CC	sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3	XX	WPI; 2000-505108/45.
CC	DNA molecule can be used for the recombinant expression of the variant.	XX	New crystals of an N-terminal fragment of a signal transducer and
CC	STAT3 protein is useful as a medicament or pharmaceutical composition for	PT	activator of transcription that effectively diffracts x-rays, useful for
CC	treatment of autoimmune or inflammatory diseases	PT	drug screening and development.
XX	Sequence 770 AA;	XX	Disclosure; Fig 1; 42pp; English.
XX	Query Match 97.9%; Score 1144; DB 2; Length 770;	XX	The present invention relates to a crystal of an N-terminal fragment of a
XX	Best Local Similarity 97.8%; Pred. No. 2.2e-96;	XX	signal transducer and activator of transcription (STAT) protein. The
XX	Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	CC	
QY	1 NHPTAAVVTKEQOMLEQHLQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60	CC	

CC crystal effectively diffracts X-rays, allowing the determination of the
CC atomic coordinates of the N-terminal domain to a resolution of greater
CC than 5.0 Angstroms. The present sequence is the N-terminal domain of the
CC murine STAT 3 protein. The N-terminal domain enables STAT dimers to
CC interact and bind DNA cooperatively, a mechanism important for gene
CC activation. The crystals are useful in drug screening and development by
CC selecting a potential drug by performing rational drug design with the 3-
CC dimensional structure determined for the crystal
XX
SQ

Sequence 770 AA;

Query Match	97.9%;	Score 1144;	DB 3;	Length 770;
Best Local Similarity	97.8%;	Pred. No. 2.2e-96;		
Matches 224;	Conservative 1;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	NHPTAAVVTKEQQMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFDNFYKTLKSGQDMQDLN	60	
Db	130	NHPTAAVVTKEQQMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFDNFYKTLKSGQDMQDLN	189	
Qy	61	GNNQSVTRQKMQQLEQMLTALDDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI	120	
Db	190	GNNQSVTRQKMQQLEQMLTALDDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQQI	249	
Qy	121	ACIGPPNICLDRLNNITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLERI	180	
Db	250	ACIGPPNICLDRLNNITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLERI	309	
Qy	181	VELFRNLKSAFVVERQPCMPHDPRLIVIKTGVPATAVALLVKFPEL	229	
Db	310	VELFRNLKSAFVVERQPCMPHDPRLIVIKTGVTTKVRLLVKFPPEL	358	

Search completed: May 25, 2005, 17:36:37
Job time : 123.057 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 28.6534 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-29
Perfect score: 1169
Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQFATAVALLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits/satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1169	100.0	229	3	US-09-387-418A-29
2	1155	98.8	229	3	US-09-387-418A-18
3	1155	98.8	229	3	US-09-387-418A-28
4	1155	98.8	252	3	US-09-387-418A-14
5	1155	98.8	271	3	US-09-387-418A-9
6	1155	98.8	770	1	US-08-369-796-12
7	1155	98.8	770	2	US-08-852-091-12
8	1155	98.8	770	2	US-08-820-754-12
9	1155	98.8	770	3	US-08-956-652-12
10	1155	98.8	770	3	US-08-956-869-12
11	1155	98.8	770	3	US-08-948-547-12
12	1155	98.8	770	3	US-09-364-970-3
13	1155	98.8	770	3	US-09-364-970-5
14	1155	98.8	770	3	US-08-956-653A-12
15	1155	98.8	770	4	US-08-212-185-12
16	1155	98.8	770	5	PCT-US95-17025-11
17	1151	98.5	229	3	US-09-387-418A-31
18	1150	98.4	229	3	US-09-387-418A-30
19	1144	97.9	770	1	US-08-416-581B-9
20	1144	97.9	770	3	US-09-012-710-8
21	1144	97.9	770	3	US-09-556-273-8
22	1144	97.9	770	3	US-09-526-542-2
23	1144	97.9	770	4	US-10-117-087-2
24	1139	97.4	770	1	US-08-416-581B-1
25	1139	97.4	770	1	US-08-416-581B-5
26	1139	97.4	770	3	US-09-087-465-6
27	1139	97.4	770	4	US-09-972-800A-6

28	1139	97.4	771	1	US-08-276-099A-14	Sequence 14, Appl
29	1139	97.4	771	1	US-08-781-890-14	Sequence 14, Appl
30	1094	93.6	213	3	US-09-387-418A-19	Sequence 19, Appl
31	1094	93.6	236	3	US-09-387-418A-15	Sequence 15, Appl
32	1027	87.9	223	3	US-09-387-418A-22	Sequence 22, Appl
33	828	70.8	185	3	US-09-387-418A-23	Sequence 23, Appl
34	781	66.8	176	3	US-09-387-418A-16	Sequence 16, Appl
35	653	55.9	128	3	US-09-387-418A-20	Sequence 20, Appl
36	605	51.8	143	3	US-09-387-418A-17	Sequence 17, Appl
37	556	47.6	268	3	US-09-387-418A-12	Sequence 12, Appl
38	556	47.6	582	4	US-09-430-806A-3	Sequence 3, Appl
39	556	47.6	712	1	US-08-369-796-6	Sequence 6, Appl
40	556	47.6	712	2	US-08-852-091-6	Sequence 6, Appl
41	556	47.6	712	3	US-08-820-754-6	Sequence 6, Appl
42	556	47.6	712	3	US-08-956-652-6	Sequence 6, Appl
43	556	47.6	712	3	US-08-956-869-6	Sequence 6, Appl
44	556	47.6	712	3	US-08-948-547-6	Sequence 6, Appl
45	556	47.6	712	3	US-08-956-653A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-387-418A-29
; Sequence 29, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Barnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-387-418A-29

Query Match		100.0%;	Score 1169;	DB 3;	Length 229;
Best Local Similarity		100.0%;	Pred No. 4e-99;		
Matches 229;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN	60		
Db	1	NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN	60		
Qy	61	GNNQSVTRQKMOQLEQMLTALQDMRRSIVSELAGLISAMEYVQKTTTDEELADMKRPEI	120		
Db	61	GNNQSVTRQKMOQLEQMLTALQDMRRSIVSELAGLISAMEYVQKTTTDEELADMKRPEI	120		
Qy	121	ACIGGPNICLDRLENNWITSLAESQLQTRQOIKLEELQOKVSYKGDPIVQHRPMLERI	180		
Db	121	ACIGGPNICLDRLENNWITSLAESQLQTRQOIKLEELQOKVSYKGDPIVQHRPMLERI	180		
Qy	181	VELFRNLMSAFVVERQPCMPHDPRLVITKGQVFATAVALLVKFPPEL	229		
Db	181	VELFRNLMSAFVVERQPCMPHDPRLVITKGQVFATAVALLVKFPPEL	229		

RESULT 2

US-09-387-418A-18
; Sequence 18, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-18

Query Match 98.8%; Score 1155; DB 3; Length 229;
Best Local Similarity 98.7%; Pred. No. 7.6e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPDFNFKTLKSGQDMODLN 60
DB 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPDFNFKTLKSGQDMODLN 60
QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
QY 121 ACIGGPPNICLDRLNENWITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
DB 121 ACIGGPPNICLDRLNENWITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
QY 181 VELFRNLKMSAFVVERQPCMPHDPDRPLVKTGVQFATAVALLVKRPPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPHDPDRPLVKTGVQFATAVALLVKRPPEL 229

RESULT 3
US-09-387-418A-28
; Sequence 28, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-28

Query Match 98.8%; Score 1155; DB 3; Length 229;
Best Local Similarity 98.7%; Pred. No. 7.6e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPDFNFKTLKSGQDMODLN 60
DB 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPDFNFKTLKSGQDMODLN 60
QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
QY 121 ACIGGPPNICLDRLNENWITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
DB 121 ACIGGPPNICLDRLNENWITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180

QY 181 VELFRNLKMSAFVVERQPCMPHDPDRPLVKTGVQFATAVALLVKRPPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPHDPDRPLVKTGVQFATAVALLVKRPPEL 229

RESULT 4

US-09-387-418A-14
; Sequence 14, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-14

Query Match 98.8%; Score 1155; DB 3; Length 252;
Best Local Similarity 98.7%; Pred. No. 8.6e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPDFNFKTLKSGQDMODLN 60
DB 24 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPDFNFKTLKSGQDMODLN 83
QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
QY 121 ACIGGPPNICLDRLNENWITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
DB 144 ACIGGPPNICLDRLNENWITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 203
QY 181 VELFRNLKMSAFVVERQPCMPHDPDRPLVKTGVQFATAVALLVKRPPEL 229
DB 204 VELFRNLKMSAFVVERQPCMPHDPDRPLVKTGVQFATAVALLVKRPPEL 252

RESULT 5

US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match 98.8%; Score 1155; DB 3; Length 271;
Best Local Similarity 98.7%; Pred. No. 9.4e-98;

Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLN 60
DB 24 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLN 83
QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB 84 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 143
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 144 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 203
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
DB 204 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 252

RESULT 6
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-369-796-12

Query Match 98.8%; Score 1155; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB 84 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 143
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 144 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 203
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
DB 204 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 252

DB 190 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 249
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
DB 310 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 358

RESULT 7
US-08-852-091-12
; Sequence 12, Application US/08852091
; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-852-091-12

Query Match 98.8%; Score 1155; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB 190 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 249
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 309

Qy 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGQFATAVALLVKFPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGQFATAVALLVKFPPEL 358

RESULT 8

US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,754
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-754-12

Query Match 98.8%; Score 1155; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTKEQMLQDLQVRRKQVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQMLQDLQVRRKQVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

Qy 61 GNNQSVTRQKMQOLEQMLTALDOMRBSIVSELAGLISAMEYVOKTLTDEELADWKRRPEI 120
Db 190 GNNQSVTRQKMQOLEQMLTALDOMRBSIVSELAGLISAMEYVOKTLTDEELADWKRRPEI 249
Qy 121 ACIGGPPNICLDRLNWNITSLAESQIQTRQIQIKKLELOKQVSYKGDPIVQHRPMLLEERI 180
Db 250 ACIGGPPNICLDRLNWNITSLAESQIQTRQIQIKKLELOKQVSYKGDPIVQHRPMLLEERI 309
Qy 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGQFATAVALLVKFPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGQFATAVALLVKFPPEL 358

RESULT 9

US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,652
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-652-12

Query Match

98.8%; Score 1155; DB 3; Length 770;


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Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDL 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDL 189
QY 61 GNNQSVTRQMKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDL 120
Db 190 GNNQSVTRQMKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDL 249
QY 121 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLELOQKVSYGKDPVQHRPMLREI 180
Db 250 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLELOQKVSYGKDPVQHRPMLREI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 358

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RESULT 10
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDL 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDL 189
QY 61 GNNQSVTRQMKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDL 120
Db 190 GNNQSVTRQMKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGDMDL 249
QY 121 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLELOQKVSYGKDPVQHRPMLREI 180
Db 250 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLELOQKVSYGKDPVQHRPMLREI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 358

RESULT 11
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 190 GNNQSVTRQKMQQLLEQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 249

QY 121 ACIGGPNICLDRLNNWITSLAESQLQTRQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNNWITSLAESQLQTRQIKKLEELQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 358

RESULT 12
US-09-364-970-3
Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-3

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 130 NHPTAAVVTKEQQLLEQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189

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QY 121 ACIGGPNICLDRLNNWITSLAESQLQTRQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNNWITSLAESQLQTRQIKKLEELQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 358

RESULT 13
US-09-364-970-5
Sequence 5, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-5

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 121 ACIGGPNICLDRLNNWITSLAESQLQTRQIKKLEELQKVS YKGDPIVQHRPMLERI 180
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DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 358

RESULT 14
US-08-956-653A-12
Sequence 12, Application US/08956653A
Patent No. 6338949
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/212,185
APPLICATION NUMBER: 11-MAR-1994
FILING DATE:

;; APPLICATION NUMBER: US 07/980,498
;; FILING DATE: 23-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/854,296
;; FILING DATE: 19-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO US93/02569
;; FILING DATE: 19-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/126,588
;; FILING DATE: 24-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-195
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-956-653A-12

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSGQDMQDLN 189

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QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 358

RESULT 15
US-08-212-185-12
; Sequence 12, Application US/08212185
; Patent No. 6605442
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/212,185
;; FILING DATE: 11-MAR-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/980,498
;; FILING DATE: 23-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/854,296
;; FILING DATE: 19-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO US93/02569
;; FILING DATE: 19-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/126,588
;; FILING DATE: 24-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-212-185-12

Query Match 98.8%; Score 1155; DB 4; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSGQDMQDLN 189

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Db 190 GNNQSVTRQKMOQLEOMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

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QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
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Search completed: May 25, 2005, 17:47:39
Job time : 28.6534 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:36:58 ; Search time 100.287 Seconds
(without alignments)
763.830 Million cell updates/sec

Title: US-10-090-185-29
Perfect score: 1169
Sequence: 1 NHPTAAVTEKQMLQHLQ.....IKTGVQFATAVALLVKEPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1155	98.8	229	13	US-10-090-185-28
4	1155	98.8	252	13	US-10-090-185-14
5	1155	98.8	271	13	US-10-090-185-9
6	1155	98.8	770	11	US-09-876-773-12
7	1155	98.8	770	17	US-10-639-617-12
8	1151	98.5	229	13	US-10-090-185-31
9	1150	98.4	229	13	US-10-090-185-30
10	1144	97.9	720	15	US-10-380-020-4
11	1144	97.9	769	15	US-10-380-020-2
12	1144	97.9	769	15	US-10-380-020-5
13	1144	97.9	770	14	US-10-045-792-8
14	1169	100.0	229	13	US-10-090-185-29
15	1155	98.8	229	13	US-10-090-185-18
16	1155	98.8	229	13	US-10-090-185-28
17	1155	98.8	252	13	US-10-090-185-14
18	1155	98.8	271	13	US-10-090-185-9
19	1155	98.8	770	11	US-09-876-773-12
20	1155	98.8	770	17	US-10-639-617-12
21	1151	98.5	229	13	US-10-090-185-31
22	1150	98.4	229	13	US-10-090-185-30
23	1144	97.9	720	15	US-10-380-020-4
24	1144	97.9	769	15	US-10-380-020-2
25	1144	97.9	769	15	US-10-380-020-5
26	1144	97.9	770	14	US-10-045-792-8

14	1144	97.9	770	14	US-10-038-010-56	Sequence 56, Appl
15	1144	97.9	770	14	US-10-117-087-2	Sequence 2, Appl
16	1144	97.9	793	9	US-09-925-302-780	Sequence 780, App
17	1144	97.9	793	10	US-09-925-302-780	Sequence 329, App
18	1141	97.6	770	15	US-10-116-275-329	Sequence 349, App
19	1139	97.4	770	15	US-10-116-275-349	Sequence 349, App
20	1094	93.6	213	13	US-10-090-185-19	Sequence 15, Appl
21	1094	93.6	236	13	US-10-090-185-15	Sequence 22, Appl
22	1027	87.9	223	13	US-10-090-185-22	Sequence 23, Appl
23	828	70.8	185	13	US-10-090-185-23	Sequence 16, Appl
24	781	66.8	176	13	US-10-090-185-16	Sequence 20, Appl
25	653	55.9	128	13	US-10-090-185-20	Sequence 17, Appl
26	605	51.8	143	13	US-10-090-185-17	Sequence 4, Appl
27	560	47.9	749	9	US-09-833-205-4	Sequence 12, Appl
28	556	47.6	268	13	US-10-090-185-12	Sequence 3, Appl
29	556	47.6	582	14	US-10-245-120-3	Sequence 6, Appl
30	556	47.6	712	11	US-09-876-773-6	Sequence 2, Appl
31	556	47.6	712	14	US-10-245-120-2	Sequence 6, Appl
32	556	47.6	712	17	US-10-639-617-6	Sequence 5, Appl
33	556	47.6	712	17	US-10-936-390-5	Sequence 2, Appl
34	556	47.6	750	9	US-09-833-205-2	Sequence 1, Appl
35	556	47.6	750	11	US-09-876-773-4	Sequence 1, Appl
36	556	47.6	750	14	US-10-245-120-1	Sequence 44, Appl
37	556	47.6	750	14	US-10-308-279-44	Sequence 352, App
38	556	47.6	750	16	US-10-755-889-352	Sequence 823, App
39	556	47.6	750	16	US-10-755-889-823	Sequence 19, App
40	556	47.6	750	17	US-10-492-043-19	Sequence 4, Appl
41	556	47.6	750	17	US-10-639-617-4	Sequence 50, App
42	556	47.6	786	9	US-09-925-297-550	Sequence 24, Appl
43	554	47.4	129	13	US-10-090-185-24	Sequence 6, Appl
44	549	47.0	749	9	US-09-833-205-6	Sequence 8, Appl
45	549	47.0	749	11	US-09-876-773-8	

ALIGNMENTS

RESULT 1
US-10-090-185-29
; Sequence 29, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 09/387,418
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 29
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-29

Query Match	100.0%	Score 1169;	DB 13;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 1.9e-94;		
Matches 229;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY 121 ACIGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
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QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKFPPEL 229
Db 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKFPPEL 229

RESULT 2

US-10-090-185-18
; Sequence 18, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-18

Query Match 98.8%; Score 1155; DB 13; Length 229;
Best Local Similarity 98.7%; Pred. No. 3.2e-93;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 3

US-10-090-185-28
; Sequence 28, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28

; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-28

Query Match 98.8%; Score 1155; DB 13; Length 229;
Best Local Similarity 98.7%; Pred. No. 3.2e-93;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLODDDFNYKTLKSGQDMODLN 60
Db 1 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLODDDFNYKTLKSGQDMODLN 60
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
QY 121 ACIGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKFPPEL 229
Db 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKFPPEL 229

RESULT 4

US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Horvath, Curt M
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 98.8%; Score 1155; DB 13; Length 252;
Best Local Similarity 98.7%; Pred. No. 3.6e-93;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLODDDFNYKTLKSGQDMODLN 60
Db 24 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLODDDFNYKTLKSGQDMODLN 83
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 84 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
QY 121 ACIGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
Db 144 ACIGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 203
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKFPPEL 229
Db 204 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKFPPEL 252

RESULT 5

US-10-090-185-9

```
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-090-185-9

Query Match          98.8%; Score 1155; DB 13; Length 271;
Best Local Similarity 98.7%; Pred. No. 3 9e-93;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDVKRKYVDLEQKMKVVENLQDDDFDNFKYTKLSQGMQDLN 60
Db 24 NHPTAAVTEKQMLEQHLQDVKRKYVDLEQKMKVVENLQDDDFDNFKYTKLSQGMQDLN 83
QY 61 GNNQSVTRQKMQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 84 GNNQSVTRQKMQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLERI 180
Db 144 ACIGGPPNICLDRLNWTSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLERI 203
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 229
Db 204 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 252

RESULT 6
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match          98.8%; Score 1155; DB 11; Length 770;
Best Local Similarity 98.7%; Pred. No. 1 5e-92;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDVKRKYVDLEQKMKVVENLQDDDFDNFKYTKLSQGMQDLN 60
Db 130 NHPTAAVTEKQMLEQHLQDVKRKYVDLEQKMKVVENLQDDDFDNFKYTKLSQGMQDLN 189
QY 61 GNNQSVTRQKMQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKMQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLNWTSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 358

RESULT 7
US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/639,617
; FILING DATE: 12-AUG-2003
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO 993/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

```

```

Query Match          98.8%; Score 1155; DB 17; Length 770;
Best Local Similarity 98.7%; Pred. No. 1.5e-92;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
Qy 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKMQOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLLEERI 180
Db 250 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLLEERI 309
Qy 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 358

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RESULT 8
US-10-090-185-31
; Sequence 31, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229

```

```

;
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-090-185-31
;
Query Match          98.5%; Score 1151; DB 13; Length 229;
Best Local Similarity 98.3%; Pred. No. 7.1e-93;
Matches 225; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Qy 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLLEERI 180
Db 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLLEERI 180
Qy 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229
Db 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229

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```

RESULT 9
US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-090-185-30

```

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Query Match          98.4%; Score 1150; DB 13; Length 229;
Best Local Similarity 98.3%; Pred. No. 8.7e-93;
Matches 225; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Qy 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLLEERI 180
Db 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLLEERI 180
Qy 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229
Db 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229

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RESULT 10
US-10-380-020-4
; Sequence 4, Application US/10380020

```


Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Dalton, William
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 720
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match 97.9%; Score 1144; DB 15; Length 720;
Best Local Similarity 97.8%; Pred. No. 1.1e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 120
DB 190 GNNQSVTRQKMQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 249
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVSYKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 358

RESULT 11
US-10-380-020-2
Sequence 2, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Dalton, William
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 769
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match 97.9%; Score 1144; DB 15; Length 769;
Best Local Similarity 97.8%; Pred. No. 1.1e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 120

DB 190 GNNQSVTRQKMQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVSYKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 358

RESULT 12
US-10-380-020-5
Sequence 5, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Dalton, William
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 769
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match 97.9%; Score 1144; DB 15; Length 769;
Best Local Similarity 97.8%; Pred. No. 1.1e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 120
DB 190 GNNQSVTRQKMQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 249
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVSYKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 358

RESULT 13
US-10-045-792-8
Sequence 8, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
CORRESPONDENCE ADDRESS: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey

;
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8

Query Match 97.9%; Score 1144; DB 14; Length 770;
Best Local Similarity 97.8%; Pred. No. 1.4e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLISAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLISAMEYVQKTLTDEELADWKRRQOI 249
QY 121 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPEL 358

RESULT 14
US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens

;
; FEATURE:
; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56
Query Match 97.9%; Score 1144; DB 14; Length 770;
Best Local Similarity 97.8%; Pred. No. 1.4e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLISAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLISAMEYVQKTLTDEELADWKRRQOI 249
QY 121 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPEL 358

RESULT 15
US-10-117-087-2
; Sequence 2, Application US/10117087
; Publication No. US20030166854A1
; GENERAL INFORMATION:
; APPLICANT: SERLUP1-CRESCENZI, Ottaviano
; APPLICANT: DELLA PIETRA, Linda
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REFERENCE: SERLUP1-2
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2

Query Match 97.9%; Score 1144; DB 14; Length 770;
Best Local Similarity 97.8%; Pred. No. 1.4e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLISAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLISAMEYVQKTLTDEELADWKRRQOI 249
QY 121 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPPEL 358

Search completed: May 25, 2005, 18:21:53
Job time : 101.62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-29
Perfect score: 1169
Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQFATAVALLVKFPPEL 229
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1144	97.9	770	2 I49508	ISGF3 p91-related
2	1139	97.4	770	2 A54444	DNA-binding protei
3	510.5	43.7	739	2 A46159	interferon-depende
4	495	42.3	748	2 A56047	gamma-interferon a
5	310	26.5	851	2 A46160	interferon alpha-1
6	269.5	23.1	786	2 I49274	mammary gland fact
7	269.5	23.1	793	2 S54772	mammary gland fact
8	263.5	22.5	794	2 G02317	transcription acti
9	238	20.4	794	2 S55527	mammary gland fact
10	126	10.8	978	2 A70387	conserved hypothet
11	124	10.6	533	2 G72593	hypothetical prote
12	122	10.4	848	2 A54740	interleukin-4-indu
13	120.5	10.3	837	2 I57557	DNA-Binding Protei
14	119.5	10.2	1166	2 T27075	hypothetical prote
15	118.5	10.1	1208	2 AE1947	chromosome segrega
16	118.5	10.1	2094	2 S33124	tpv protein - huma
17	115.5	9.9	924	2 S06117	myosin heavy chain
18	115	9.8	1164	2 T24806	hypothetical prote
19	114.5	9.8	2007	1 B43402	myosin heavy chain
20	114	9.8	1976	2 A59252	myosin heavy chain
21	113.5	9.7	727	2 AC1814	hypothetical prote
22	113.5	9.7	857	2 S33821	median body protei
23	112.5	9.6	946	2 S28061	SCP1 protein - rat
24	112.5	9.6	1690	2 T13030	microtubule bindin
25	112.5	9.6	1957	2 T38077	hypothetical coile
26	112.5	9.6	2253	2 T30336	nuclear/mitotic ap
27	112	9.6	289	2 S51193	epimorphin - mouse
28	112	9.6	1509	1 A27224	myosin heavy chain
29	112	9.6	1999	1 S21801	myosin heavy chain

30	111.5	9.5	284	2 C64527	M protein - Helico
31	111.5	9.5	1048	1 BVSCSC	exonuclease (EC 3.
32	111	9.5	1959	1 A33977	myosin heavy chain
33	110.5	9.5	747	1 A57107	kinesin-related pr
34	110.5	9.5	1940	1 A59287	myosin heavy chain
35	110.5	9.5	1992	2 A47297	myosin heavy chain
36	110	9.4	1188	2 G83960	chromosome segrega
37	110	9.4	2020	2 T21174	hypothetical prote
38	109.5	9.4	434	2 T43448	hypothetical prote
39	109.5	9.4	527	2 S33068	myosin heavy chain
40	109.5	9.4	734	2 T27055	hypothetical prote
41	109.5	9.4	896	2 S43074	epidermal growth f
42	109.5	9.4	1047	2 C85535	ATP-dependent dsDN
43	109.5	9.4	1047	2 G90684	ATP-dependent dsDN
44	109.5	9.4	1738	2 T14867	interaptin - slime
45	109.5	9.4	3685	1 A27605	dystrophin, muscle

ALIGNMENTS

RESULT 1

I49508

ISGF3 p91-related transcription factor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49508; I49009

R:Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su

Cell 77, 63-71, 1994

A>Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr

A:Reference number: A54444; MUID:94208062; PMID:7512451

A:Accession: I49508

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-770 <RES>

A:Cross-references: UNIPROT:P42227; GB:I29278; NID:G476715; PIDN:AAA37254.1; PID:G47671

R:Kaz, R.; Durbin, J.E.; Levy, D.E.

J. Biol. Chem. 269, 24391-24395, 1994

A>Title: Acute phase response factor and additional members of the interferon-stimulate

A:Reference number: I49009; MUID:95014185; PMID:7523373

A:Accession: I49009

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-393, 'M', 395-700, 702-770 <RE2>

A:Cross-references: EMBL:U08378; NID:G473889; PIDN:AAA56668.1; PID:G473890

C:Genetics:

A:Gene: APRF

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 97.9%; Score 1144; DB 2; Length 770;

Best Local Similarity 97.8%; Pred. No. 1e-68;

Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQMKVVENLQDDPFNYKTLKSGQDMQDLN 60

Db 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQMKVVENLQDDPFNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMOOLEQMLTALDOMERSIVSELAGLLSAMEYVQKTLTDESLADWKRPEI 120

Db 190 GNNQSVTRQKMOOLEQMLTALDOMERSIVSELAGLLSAMEYVQKTLTDESLADWKRQOI 249

QY 121 ACIGGPPNICLDRLENWITSLAESQLQTRQQLKCLEELQKQVSYKGDPTVQHRPMLERI 180

Db 250 ACIGGPPNICLDRLENWITSLAESQLQTRQQLKCLEELQKQVSYKGDPTVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 229

Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 358

RESULT 2

A54444

DNA-binding protein APRF - human

A;Reference number: S53873; MUID:95192056; PMID:7885841

A;Accession: S53873

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-196;392-591;684-730 <YAW>

A;Cross-references: EMBL:U18671

C;Genetics:

A;Gene: stat2

A;Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 40

C;Superfamily: human signal transducer and transcription activator STAT5A

C;Keywords: signal transduction; transcription regulation

Query Match 26.5%; Score 310; DB 2; Length 851;

Best Local Similarity 32.8%; Pred. No. 3.7e-13;

Matches 72; Conservative 51; Mismatches 92; Indels 6; Gaps 4;

QY 8 VTEKQQLQHLQDVRKRVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNQSVT 67

DB 138 VESQHEISRIIDLAMWEKLVKSIQLXQDDVCFRYK-IOAGKTPSLDPH--QTK 194

QY 68 RQMQQLQHLQDVRKRVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNQSVT 127

DB 195 EQKI--LQETNELDKRRKEVLDASKALLGRLLFTLIELLL-PKLEWKAQQQKACIRAPI 251

QY 128 NCLDRLNWLITSLAESQLOTRQIKKLEELQKQVSKGDPVVOHRPMLERIVELFRML 187

DB 252 DHGLEQLFTWFTAGAKLLFHLRLKELKGLSLVSYQDDPLTKGVDLRNAQVTELLORL 311

QY 188 MKSAFVVERQPCMPHDPRLVTKTGQFATAVALLVKPE 228

DB 312 LHRAFVVERQPCMPQTPHRLIKTKGKFTVTRLLVRLQE 352

RESULT 6

I49274

mammary gland factor - mouse

N;Alternate names: STAT5 protein homolog p80

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49274; S54773

R;Liu, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in

A;Reference number: I49273; MUID:96004632; PMID:7568026

A;Accession: I49274

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-786 <RES>

A;Cross-references: UNIPROT:P42232; UNIPROT:Q9UKM1; EMBL:U21110; NID:g747973; PIDN:AA052

R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A;Reference number: S54772; MUID:95237198; PMID:7720707

A;Accession: S54773

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-432,'E',434-786 <MUI>

A;Cross-references: EMBL:248539; NID:g758635; PIDN:CAA88420.1; PID:g758636

R;Azam, M.; Erdjument-Bronage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,

EMBO J. 14, 1402-1411, 1995

A;Title: Interleukin-3 signals through multiple isoforms of Stat5.

A;Reference number: S54725; MUID:95246733; PMID:7537213

A;Accession: S54727

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-432,'E',434-786 <AZA>

C;Genetics:

A;Gene: Stat5b

C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 23.1%; Score 269.5; DB 2; Length 786;

Best Local Similarity 30.6%; Pred. No. 1.7e-10;

Matches 71; Conservative 42; Mismatches 98; Indels 21; Gaps 5;

QY 5 AAVVTEKQQLQHLQDVRKRVDLEQKMKVVENLQDDFDNFY-KTLKSGQDMQDLNGNN 63

DB 134 ADAMSQKHLQINQTFEELRLITQDTENELKQLQQTQBYFIQYQESLRIOAQAQLGQLN 193

QY 64 -----QSVTRQKMQQLQEQML-----TALDQMRRSIVSELAGLLSMEYVQKTLTDEELA 112

DB 194 POERMSRETALQKQVSLTQWQREAOITQQYRVLAELAEKHQKTLQLLRKQQTILDDLEI 253

QY 113 DWKRRPEIACIGPPNCLDRLENWITSLAESQLOTRQIKKLEELQKQVSKGDPVVOHRP 172

DB 254 QWKRRQQLAGNGPPGSLDLVQSWCEKLAETIWNQRIIRRAEHLCCQLPIFG-PVEEM 312

QY 173 RPLMEERIVELFRMLMKSAPVVERQPCMPHDPRLVTKTGQFATAVALLV 224

DB 313 LAEVNATITDIISALVTSTFIEKQP-----PQVLTKQTKFAATVRLVV 356

RESULT 7

S54772

mammary gland factor - mouse

N;Alternate names: stat5 protein

C;Species: Mus musculus (house mouse)

C;Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S54772; I49273

R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A;Reference number: S54772; MUID:95237198; PMID:7720707

A;Accession: S54772

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-793 <MUI>

A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA8

R;Liu, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved

A;Reference number: I49273; MUID:96004632; PMID:7568026

A;Accession: I49273

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-793 <RES>

A;Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972

C;Genetics:

A;Gene: Stat5a

C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 23.1%; Score 269.5; DB 2; Length 793;

Best Local Similarity 30.6%; Pred. No. 1.7e-10;

Matches 70; Conservative 42; Mismatches 96; Indels 21; Gaps 5;

QY 8 VTEKQQLQHLQDVRKRVDLEQKMKVVENLQDDFDNFY-KTLKSGQDMQDLNGNN--- 63

DB 137 MSQKHLQINQRFEEELRLITQDTENELKQLQQTQBYFIQYQESLRIOAQAQLGQLN 196

QY 64 -----QSVTRQKMQQLQEQML-----TALDQMRRSIVSELAGLLSMEYVQKTLTDEELADWK 115

DB 197 RMSRETALQKQVSLTQWQREAOITQQYRVLAELAEKHQKTLQLLRKQQTILDDLEI 256

QY 116 RPETIACIGPPNCLDRLENWITSLAESQLOTRQIKKLEELQKQVSKGDPVVOHRPM 175

DB 257 RRQQLAGNGPPGSLDLVQSWCEKLAETIWNQRIIRRAEHLCCQLPIFG-PVEMLAE 315

QY 176 LEERIVELFRMLMKSAPVVERQPCMPHDPRLVTKTGQFATAVALLV 224

DB 316 VNATITDIISALVTSTFIEKQP-----PQVLTKQTKFAATVRLVV 356

RESULT 8

G02317

transcription activator stat5a - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G02317
R;Lin. J.
Submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g1151169
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.5%; Score 263.5; DB 2; Length 794;
Best Local Similarity 30.1%; Pred. No. 4.3e-10;
Matches 69; Conservative 43; Mismatches 96; Indels 21; Gaps 5;

Qy 8 VTEKQMLEQHLQDVRKRVQDLQKMKVENVLQDDFDNFY-KTLKSGDQMDL----- 59
Db 137 MSQKHLQNTQFEELRLVTDTENELKLOQTQYFIQYQESLRIOQAQFAQLSPQE 196
Qy 60 NGNNQSVTRQKMOLEQML-----TALDOMRSIVSELAGLSAMEYVQKTLTDEELADWK 115
Db 197 RLSRETALQKQVSLQVLEAWLQREAGTLOQYRVLEAEKHQKTLQLLRKQKQTLIDDELIQWK 256
Qy 116 RRPFIACIGPPNCLDRLENWITSLSAQSLQTRQKQKLEELQKQVSKYKGDPIVQHRPM 175
Db 257 RRQLAGNGPPGSLDVLQSWCKEKLAEIITWQNRQRIIRRAEHLCCQLPIFG-PVEEMLAE 315
Qy 176 LEERIVELFRLNLMKSAFVVERQPCMPHDPRLVKTGVQFATAVALLV 224
Db 316 VNATITDIISALVTSTFIEIKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 9
S55527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regulat
A;Reference number: S55527; MUID:9518889; PMID:7892987
A;Accession: S55527
A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:9602354; PIDN:CAA55191.1; PID:g6023
A;Note: This is a revision to the sequence from reference S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716, 'RHLHGSGLSPR', 729, 'P', 731, 'ASL', <WAW>
A;Cross-references: EMBL:X78428
A;Note: This sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.4%; Score 238; DB 2; Length 794;
Best Local Similarity 29.3%; Pred. No. 2.1e-08;
Matches 67; Conservative 42; Mismatches 98; Indels 22; Gaps 6;

Qy 8 VTEKQMLEQHLQDVRKRVQDLQKMKVENVLQDDFDNFY-KTLKSGDQMDLNGNN--- 63
Db 138 MSQKHLQNTQFEELRLVTDTENELKLOQTQYFIQYQESLRIOQAQFAQLNPQE 197
Qy 64 ----QSVTRQKMOLEQML-----TALDOMRSIVSELAGLSAMEYVQKTLTDEELADWK 115
Db 198 RLSRETALQKQVSLQVLEAWLQREAGTLOQYRVLEAEKHQKTLQLLRKQKQTLIDDELIQWK 257
Qy 116 RRPFIACIGPPNCLDRLENWITSLSAQSLQTRQKQKLEELQKQVSKYKGDPIVQHRPM 175
Db 258 RRHDWRGMEAPPR-SLDVLQSWCKEKLAEIITWQNRQRIIRRAEHLCCQLPIFG-PVEEMLAE 315

Qy 176 LEERIVELFRLNLMKSAFVVERQPCMPHDPRLVKTGVQFATAVALLV 224
Db 316 VNATITDIISALVTSTFIEIKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 10
A70387
conserved hypothetical protein aq_1006 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70387
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70387
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-978 <AQF>
A;Cross-references: UNIPROT:O67124; GB:AE000718; NID:g2983504; PIDN:AAC07092.1; PID:g29
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1006
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 10.8%; Score 126; DB 2; Length 978;
Best Local Similarity 23.8%; Pred. No. 0.77;
Matches 50; Conservative 38; Mismatches 80; Indels 42; Gaps 6;

Qy 10 EKQMLEQHLQDVRKRVQDLQKMKVENVLQDDFDNFYKTLKSGDQMDLNGNNSVTRQ 69
Db 234 EEKDSLERLSQVVTYKLELENLEKEVEKLEKLEFSRVAP-----YVPIAK 281
Qy 70 KMOQLQMLTALDOMRSIVSELAGLSAMEYVQKTLT-----DEELAD- 113
Db 282 RIEIDKKLTTELKVRKNKLTKEALVLDKLSLPAEELNRIEAEKFEKEKEKELEHR 341
Qy 114 WKRPFIACIGPPNCLDRLENWITSLSAQSLQTRQKQKLEELQKQVSKYKGDPIVQHR 173
Db 342 LKKLQIKRI-----LKELSQLSSLSKEKEKEVEKQEFEDLSERVE-KGKKLVAET 393
Qy 174 PMLERIVELFRN-----LMKSAFVVERQ 197
Db 394 BEKLEKIKELFSEBEYTSKMKERLILVELQ 423

RESULT 11
G72593
hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72593
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-533 <KAW>
A;Cross-references: UNIPROT:Q9YCP2; DDBJ:AF000061; NID:g5104821; PIDN:BAAB0205.1; PID:
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1216

Query Match 10.6%; Score 124; DB 2; Length 533;
Best Local Similarity 21.2%; Pred. No. 0.52;
Matches 42; Conservative 49; Mismatches 65; Indels 42; Gaps 7;

Qy 8 VTEKQMLEQHLQDVRKRVQDLQKMKVENVLQDDFDNFY-----LQDDF-----DFNYK 48

Db 319 MSQQLALAEEDLESRRVEDLEARVGSVEDRLSQAEEIDSLTTSLSLRTELEDLSR 378
QY 49 TLKSGQDMQDLNGNNSVTRQKMQQLQEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTD 108
Db 379 LAEAQASLEDNTRLDQVA-STLQQLQQRALTAEEISLQALTEDLASLQAEVETLQQSIVE 437
QY 109 BELADWKRPRPIACIGPPNICLDRLNWTSLAESQLQ-----TROQIKKLEELQKQVSY 164
Db 438 IDRLQLRLSTVDV-----RLE--VESLGEKLVAQAEKNQRQDASIEDFQSIQ- 485
QY 165 KGDPVQHRPMLREIVE 182
Db 486 -----ELRQLDEKTR 497

RESULT 12

A54740
interleukin-4-induced transcription factor stat - human
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: A54740
R:Hou, J.; Schindler, U.; Henszel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A:Title: An interleukin-4-induced transcription factor: IL-4 stat.
A:Reference number: A54740; MUID:94367369; PMID:8085155
A:Accession: A54740
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-848 <HOU>
A:Cross-references: UNIPROT:P42226
A:Superfamily: human signal transducer and transcription activator STAT5A
C:Keywords: DNA binding; transcription regulation

Query Match 10.4%; Score 122; DB 2; Length 848;
Best Local Similarity 24.3%; Pred. No. 1.2; Indels 50; Gaps 9;
Matches 58; Conservative 37; Mismatches 94
QY 3 PTAAVVTEKQMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLNGN 62
Db 92 PLKLVA-----PRQILQKKAV-----MEQFRHLPWFPHWKQELKFKTGLRLQHR 140
QY 63 NQSV--TRQKMQ-----LEQML-----TALDQMRRSIVSELAGLLSAMEYVQKTL 106
Db 141 VGEIHLLREALQKAGABAGVSLHSLETPTANGTGPSEALMLQIETTGELEA-----AKAL 196
QY 107 TDELDWKRPRPIACIGPPNICLDRLNWTSLAESQLQEQMLTALDQMRRSIVSELAGLLSAMEY 166
Db 197 VLKRIQIWRKQQQLAGNAP-----FEESLAPQERCSLVDIYSQLQQRVGAAG 246
QY 167 DPI-VQHRPMLREIVELEFNLKMSAFVVERQPCMPHDPRLVKTGQFATAVALLV 224
Db 247 GELEPKTRASLTGLDEVLTIVTSFELVEKQP-----FQVLKTKYKFGQVGRFLL 297

RESULT 13

I57557
DNA-Binding Protein and transcription factor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I57557
R;Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleve
Mol. Cell. Biol. 15, 3336-3343, 1995
A:Title: Cloning of murine Stat6 and human Stat6. Stat proteins that are tyrosine phosph
A:Reference number: I57557; MUID:95280934; PMID:7760829
A:Accession: I57557
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-837 <RES>
A:Cross-references: UNIPROT:P52633; GB:I47650; NID:g1008876; PID:AAA79006.1; PID:g10088
C:Genetics: AE1947
A:Gene: STAT6
C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 10.3%; Score 120.5; DB 2; Length 837;
Best Local Similarity 25.8%; Pred. No. 1.5; Indels 59; Gaps 10;
Matches 60; Conservative 31; Mismatches 83
QY 10 EKQOMLEQ--HLQDVVRKRVQD-----LEQKMKVVENLQDDDFNFYKTLKSGQDMQ 57
Db 106 EKAVIEEPRHLPQGFHRKQEBLKFTYPLGRLLHVRRETRLLRESHLGPKT--GQVSLQ 163
QY 58 D-----LNGNNSVTRQKMQQLQEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELA 112
Db 164 NLIDPELNGPGFS-----EDLPTILQ-----GTVGDLTTQ-PLVLLRIQ 202
QY 113 DWKRPRPIACIGPPNICLDRLNWTSLAESQLQEQMLTALDQMRRSIVSELAGLLSAMEYVQKGPVIVQ 171
Db 203 IWKROQQLAGNCTPFEEISLAGLQERCELSVEIYSQLHQBGAASGELEPKT----- 253
QY 172 HRPMLREIVELEFNLKMSAFVVERQPCMPHDPRLVKTGQFATAVALLV 224
Db 254 -RASLSRDEVLRTLVTSFELVEKQP-----FQVLKTKYKFGQVGRFLL 297
RESULT 14
T27075
hypothetical protein Y51A2D.16 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27075
R:McMurray, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20307
A:Accession: T27075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1166 <WIL>
A:Cross-references: EMBL:AL021497; PIDN:CAA16403.1; GSPDB:GN00023; CESP:Y51A2D.16
A:Experimental source: clone Y51A2D
C:Genetics:
A:Map position: 5
A:Introns: 17/3; 45/1; 76/2; 156/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 94

Query Match 10.2%; Score 119.5; DB 2; Length 1166;
Best Local Similarity 21.4%; Pred. No. 2.6; Indels 73; Gaps 9;
Matches 52; Conservative 46; Mismatches 72
QY 1 NHPTAAVTEKQ-----QMLEQHLQD-----VRKRVQDLEQKMKVVENLQDD 42
Db 430 SHVTRSLSEKTKLAKLLE--LQDQVEAQTLLELNQKCGKRLERDQMSLNHLKNE 487
QY 43 FDFNYKTLKSGQDMQDLNGNNSVTRQKMQQLQEQMLTALDQMRRSIVSELAGLLSAMEY- 101
Db 488 LENDLTKCTQTOLELES-----KKLQRLREDLVLEKSRREADLIGRIHSICTTTLN 537
QY 102 ---VQKTLTDEELAD-----WKRPRPIACIGPPNI----- 129
Db 538 GANFEKINDDDELIDNIDIMNALVAVKRERDDLRIQGNQOIQELHDLKRDIEKLRSR 597
QY 130 --CLDLELWNITSLAESQLQEQMLTALDQMRRSIVSELAGLLSAMEY- 183
Db 598 SSLSNESDRVRELTRENHMTKEQVPMQLQERLNLSTKNDI-----DMVKASIEEL 653
QY 184 FRN 186
Db 654 NRN 656

RESULT 15

AE1947
chromosome segregation protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C/Superfamily: chromosome segregation protein SMC1

153 -----KKLEELQKQV-SYKGDPIVQHRPMLERIVELFRNLKMSAF 192

Search completed: May 25, 2005, 17:45:28
Job time : 22.6038 secs

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimdon J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RN SEQUENCE OF 564-704 FROM N.A.
 RP TISSUE=Liver;
 RC Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
 RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 [6]
 RN PHOSPHORYLATION ON SERINE
 RX MEDLINE=95215843; PubMed=7701321;
 RA Zhang X., Bienis J., Li H.-C., Schindler C., Chen-Kiang S.;
 RT "Requirement of serine phosphorylation for formation of STAT-promoter
 RT complexes.";
 Science 267:1990-1994(1995).
 [7]
 RN INTERACTION WITH NCOAL
 RP PubMed=1173079; DOI=10.1074/jbc.M11486200;
 RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
 RT "Functional interaction of STAT3 transcription factor with the
 RT coactivator NcoA/SRC1a.";
 J. Biol. Chem. 277:8004-8011(2002).
 CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes.
 CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P40763-1; Sequence=Displayed;
 CC Name=Del-701;
 CC IsoId=P40763-2; Sequence=VSP_010474;
 CC -1- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
 CC muscle, kidney and pancreas.
 CC -1- PM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity.
 CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -----
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 CC -----
 DR EMBL; L29277; AAA58374.1; -;
 DR EMBL; AJ012463; CAA10032.1; -;
 DR EMBL; AY572796; AAG66986.1; -;
 DR EMBL; BC000627; AAH00627.1; -;
 DR EMBL; BC014482; AAH14482.1; -;
 DR EMBL; AF029311; AAB84254.1; -;
 DR PIR; A54444; A54444.
 DR HSSP; P42227; 1BG1.
 DR TRNSPAC; T01493; -;
 DR Genew; HGNC:11364; STAT3.
 DR H-TnVDB; HIX0013840; -;
 DR MM; 102582; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
 DR GO; GO:0000122; P:negative regulation of transcription from P. . .; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR PROSITE; PS0001; SH2; 1.
 KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
 KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
 FT DOMAIN 580 670
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (by similarity).
 FT MOD_RES 727 727 Phosphoserine (by similarity).
 FT VARSPLIC 701 701 Missing (in isoform Del-701).
 FT FTId=VSP_010474.
 FT VARIANT 32 32 Q -> K (in dbSNP:1803125).
 FT FTId=VAR_018683.
 FT VARIANT 143 143 M -> I.
 FT FTId=VAR_018679.
 FT CONFLICT 288 288 Q -> H (in Ref. 1).
 FT CONFLICT 460 460 P -> S (in Ref. 1).
 FT CONFLICT 548 548 K -> N (in Ref. 1).
 FT CONFLICT 561 561 F -> Y (in Ref. 1).
 FT CONFLICT 667 667 V -> L (in Ref. 1).
 FT CONFLICT 730 730 T -> A (in Ref. 1).
 SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
 Query Match 97.9%; Score 1144; DB 1; Length 770;
 Best Local Similarity 97.8%; Pred. No. 4.3e-62;
 Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQQLQHLQDVVKRQVQDLQKMKVVENLQDDFDNFYKTLKSGQMDLN 60
 DB 130 NHPTAAVTEKQQLQHLQDVVKRQVQDLQKMKVVENLQDDFDNFYKTLKSGQMDLN 189
 QY 61 GNNQSVTRQMQQQLQDLQKMKVVENLQDDFDNFYKTLKSGQMDLN 120
 DB 190 GNNQSVTRQMQQQLQDLQKMKVVENLQDDFDNFYKTLKSGQMDLN 249
 QY 121 ACIGGPNICLDLENWITSLAESQIQTRQIQKLELQKQVSKGDPVQHRPMLERI 180
 DB 250 ACIGGPNICLDLENWITSLAESQIQTRQIQKLELQKQVSKGDPVQHRPMLERI 309
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGQFATAVALVKPPEL 229
 DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGQFATAVALVKPPEL 358
 RESULT 2
 STAJ MOUSE
 ID STAJ3 MOUSE STANDARD; PRT; 770 AA.
 AC P42227;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 GN Name-Stat3; Synonyms=Aprf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
 RP AND 632-640.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;

RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RL Cell 77:63-71 (1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Thymus;
RX MEDLINE=94188718; PubMed=8140422;
RA Zhong Z., Wen Z., Darnell J.E. Jr.;
RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
RT response to epidermal growth factor and interleukin-6.";
RL Science 264:95-98 (1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Brain;
RX MEDLINE=95014185; PubMed=7523373;
RA Raz R., Durbin J.E., Levy D.E.;
RT "Acute phase response factor and additional members of the interferon-
RT stimulated gene factor 3 family integrate diverse signals from
RT cytokines, interferons, and growth factors.";
RL J. Biol. Chem. 269:24391-24395 (1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
RX MEDLINE=96016116; PubMed=7568080;
RA Schaefer T.S., Sanders L.K., Nathans D.;
RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
RT form of Stat3.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101 (1995).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=129/SVJ;
RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
RA Miyoshi K., Cui Y., Riedinger G., Lehoczy J., Zon L., Oka T.,
RA Dewar K., Hennighausen L.;
RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
RT zebrafish to mouse.";
RL Genomics 71:150-155 (2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=C57BL/6J, and NOD/LtJ;
RA Davoodi-Semlomi A., She J.-X.;
RT "A mutant Stat5b with weaker DNA binding defines a key defective
RT pathway in non-obese diabetic (NOD) mice.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.

RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
RA Wen Z., Zhong Z., Darnell J.E. Jr.;
RT "Maximal activation of transcription by Stat1 and Stat3 requires both
RT tyrosine and serine phosphorylation.";
RL Cell 82:241-250 (1995).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
RA Becker S., Groner B., Mueller C.W.;
RT "Three-dimensional structure of the Stat3beta homodimer bound to
RT DNA.";
RL Nature 394:145-151 (1998).
CC -|- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes. STAT3B interacts with the N-terminal
CC part of JUN to activate such promoters in a cooperative way.
CC -|- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -|- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (by similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Stat3a;
CC IsoId=P42227-1; Sequence=Displayed;
CC Name=Stat3b;
CC IsoId=P42227-2; Sequence=VSP_006287;
CC Name=Del-701;
CC IsoId=P42227-3; Sequence=VSP_010475;
CC -|- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
CC kidney. STAT3B is also detected in the liver, although in a much
CC less abundant manner.
CC -|- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -|- SIMILARITY: Belongs to the transcription factor STAT family.
CC -|- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC -----
DR EMBL; L29278; AAA37254.1; --
DR EMBL; U06922; AAA19452.1; --
DR EMBL; U08378; AAA56668.1; --
DR EMBL; U30709; AAC52612.1; --
DR EMBL; AF246978; AAL59017.1; --
DR EMBL; AY299489; AAO75418.1; --
DR EMBL; AY299490; AAO75419.1; --
DR EMBL; BC003806; AAH03806.1; --
DR FIR; I49508; I49508.
DR PDB; 1BG1; X-ray; A=1-722.
DR TRANSFAC; T01574; --
DR MGD; MGI:103039; Stat3.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0003677; F:DNA binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0015563; F:transcriptional activator activity; IDA.
DR GO; GO:0007259; P:JAK-STAT cascade; IDA.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.

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DR PFam; PF02865; STAT int; 1.
DR PROSITE; PS50001; SH2; 1.
KW 3D-structure; Activator; Acute phase; Alternative splicing;
KW Direct protein sequencing; DNA-binding; Nuclear protein;
KW Phosphorylation; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD RES 727 727 Phosphoserine
FT VARSPIC 716 770
FT TCSNTYDLMSPRTLSLMQFGNNGGASPSAGGQFESLT
FT FMDLDTSECATSPM -> FIDAVWK (in isoform
FT Stat3B).
FT FTTid=VSP_006287.
FT Missing (in isoform Del-701).
FT FTTid=VSP_010475.
FT VARSPIC 701 701
FT MUTAGEN 727 727 S->A: Decreased transcriptional
FT activation.
FT CONFLICT 16 16 E -> K (in Ref. 2).
FT CONFLICT 25 25 S -> T (in Ref. 2 and 4).
FT CONFLICT 394 394 M -> I (in Ref. 1).
FT HELIX 139 180
FT TURN 181 182
FT TURN 197 198
FT HELIX 199 237
FT TURN 238 238
FT TURN 239 251
FT TURN 252 253
FT HELIX 261 290
FT TURN 294 295
FT TURN 297 301
FT TURN 302 320
FT HELIX 321 328
FT STRAND 330 331
FT TURN 333 334
FT TURN 336 337
FT STRAND 338 340
FT TURN 341 342
FT STRAND 345 351

Query Match 97.9%; Score 1144; DB 1; Length 770;
Best Local Similarity 97.8%; Pred. No. 4.3e-62;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTKEQMLEQHLQDVVKRQVQDLQKMKVVENLQDDFDNFYKTKLSQGDMDLN 60
Db 130 NHPTAAVVTKEQMLEQHLQDVVKRQVQDLQKMKVVENLQDDFDNFYKTKLSQGDMDLN 189

Qy 61 GNNQSVTRQMKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEBLADWKRRPEI 120
Db 190 GNNQSVTRQMKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEBLADWKRRQOI 249

Qy 121 ACIGGPPNICLDLENWITSLSAESQLQTRQIKKLELOQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDLENWITSLSAESQLQTRQIKKLELOQKVS YKGDPIVQHRPMLERI 309

Qy 181 VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFATAVALIVKFPPEL 229
Db 310 VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFATAVALIVKFPPEL 358

RESULT 3
STA3 RAT
ID -STA3 RAT STANDARD; PRT; 770 AA.
AC PS2631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=Stat3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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RESULT 4

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STA3_BOVIN          STANDARD;          PRT;          770 AA.
ID  STA3_BOVIN
AC  P61635;
DT  05-JUL-2004 (Rel. 44, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last sequence update)
DE  Signal transducer and activator of transcription 3.
DE  Signal transducer and activator of transcription 3.
GN  Name=STAT3;
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Mammary gland;
RA  Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RT  "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
RT  during ruminant evolution.";
RL  Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC  (IL-6)-responsive elements identified in the promoters of various
CC  acute-phase protein genes (By similarity).
CC  -!- PATHWAY: Involved in the gpl30-mediated signaling pathway.
CC  -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC  member (at least STAT1). Interacts with NCOAL (By similarity).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC  in response to phosphorylation (By similarity).
CC  -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC  -!- SIMILARITY: Contains 1 SH2 domain.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/annouce/
CC  or send an email to license@isb-sib.ch).
CC  -----
EMBL; AJ620655; CAP06182.1; -.
DR  PROSITE; PS5001; SH2; 1
KW  Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW  Transcription regulation.
FT  DOMAIN 580 670 SH2.
FT  MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT  MOD_RES 727 727 Phosphoserine (By similarity).
SQ  SEQUENCE 770 AA; 87974 MW; 9CEB147C7383274 CRC64;

Query Match 97.3%; Score 1137; DB 1; Length 770;
Best Local Similarity 97.4%; Pred. No. 1.1e-61;
Matches 223; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQMKQMLEQMLTALDQRRSIVSELQGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQMKQMLEQMLTALDQRRSIVSELQGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVKSGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVKSGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALLVKFPPEL 358

RESULT 5
Q6DV79
ID Q6DV79
AC Q6DV79;          PRELIMINARY;          PRT;          771 AA.

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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Signal transducer and activator of transcription 3.
DE Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641397; AAT64887.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match 95.7%; Score 1119; DB 2; Length 771;
Best Local Similarity 96.1%; Pred. No. 1.5e-60;
Matches 219; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 HPTAAVTEKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 61
DB 131 HPTAAVTEKQOMLEQHLQDVQRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 190
QY 62 NNSQSVTRQMKQMLEQMLTALDQRRSIVSELQGLLSAMEYVQKTLTDEELADWKRPEIA 121
DB 191 NNSQSVTRQMKQMLEQMLTALDQRRSIVSELQGLLSAMEYVQKTLTDEELADWKRPEIA 250
QY 122 CIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVKSGDPIVQHRPMLERI 181
DB 251 CIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVKSGDPIVQHRPMLERI 310
QY 182 ELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALLVKFPPEL 229
DB 311 ELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALLVKFPPEL 358

RESULT 6
O9PVX8          PRELIMINARY;          PRT;          769 AA.
ID  O9PVX8
AC  O9PVX8;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Stat 3.
GN  Name=stat 3;
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
RA Asashima M., Yokota T.;
RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
RT embryos independent of BMP-4.";
RL Dev. Biol. 216:481-490 (1999).
DR EMBL; AB017701; BAA86061.1; -.

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DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:intracellular signaling cascade; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000980; SH2_1.
DR InterPro; IPR000980; SH2_2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF001017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;

Query Match 92.9%; Score 1086; DB 2; Length 769;
Best Local Similarity 91.7%; Pred. No. 1.5e-58;
Matches 210; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 130 SHPNAAVTEKQOMLEQHLQDVVRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDLSELN 189
QY 61 GNNQSVTRQMKQMLEQHLQDVVRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 120
Db 190 GNNQSVTRQMKQMLEQHLQDVVRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDLSELN 249
QY 121 ACIGGPPNICLDLENWITSLSAESQLQTRQIQIKLEELQKVKSGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDLENWITSLSAESQLQTRQIQIKLEELQKVKSGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPFEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATKVRLLVVKPFEL 358

RESULT 7
Q7ZKX3 PRELIMINARY; PRT; 766 AA.
AC Q7ZKX3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3-A protein.
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=22348257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
Dev. Dyn. 225:384-391(2002).
[3]
SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044717; AAH44717.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;

Query Match 92.8%; Score 1083; DB 2; Length 766;
Best Local Similarity 90.8%; Pred. No. 2.3e-58;
Matches 208; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 130 SHPNAAVTEKQOMLEQHLQDVVRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDLSELN 189
QY 61 GNNQSVTRQMKQMLEQHLQDVVRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 120
Db 190 GNNQSVTRQMKQMLEQHLQDVVRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDLSELN 249
QY 121 ACIGGPPNICLDLENWITSLSAESQLQTRQIQIKLEELQKVKSGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDLENWITSLSAESQLQTRQIQIKLEELQKVKSGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPFEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATKVRLLVVKPFEL 358

RESULT 8
Q7ZTS5 PRELIMINARY; PRT; 414 AA.
AC Q7ZTS5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;

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Matches 192; Conservative 21; Mismatches 15; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDVRRVQDLEQKMKVVENLQDDFDNFYKTLKSQDGM-QDLN 60
Db 130 HPTGTVTEKQMLEHNLQDVRKQVDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDLN 189
QY 61 GNNQ-SVTRQKMQQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLTALDQRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 13
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0003700; F:intracellular signaling cascade; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF02864; STAT_alpha; 1.
DR Pfam; PF02865; STAT_bind; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFE18BEFD8BE CRC64;

Query Match 83.3%; Score 974; DB 2; Length 764;
Best Local Similarity 82.3%; Pred. No. 1.1e-51;
Matches 189; Conservative 21; Mismatches 18; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDVRRVQDLEQKMKVVENLQDDFDNFYKTLKSQDGM-QDLN 60
Db 130 NPSGTVTEKQMLENLQDVRKQVDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDLN 189
QY 61 GNNQ-SVTRQKMQQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLTALDQRRQIVTEMAGLLTAMDYVQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 14
Q13133 PRELIMINARY; PRT; 767 AA.
AC Q13133;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
GN Names=rbStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0003700; F:intracellular signaling cascade; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_Bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match 82.5%; Score 964; DB 2; Length 767;
Best Local Similarity 80.1%; Pred. No. 4.6e-51;
Matches 185; Conservative 25; Mismatches 19; Indels 2; Gaps 2;
QY 1 NHPTAAVTEKQMLEQHLQDVRRVQDLEQKMKVVENLQDDFDNFYKTLKSQDGM-QDL 59
Db 129 SHPSGTVTEKQMLEHNLQDVRKQVDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDM 188
QY 60 GNNQ-SVTRQKMQQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
Db 189 NGNSQAARQKMAQLEQMLTALDQRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 248
QY 119 ETACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 178
Db 249 QIACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 308
QY 179 RIVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 309 KIVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 15
Q9N145 PRELIMINARY; PRT; 163 AA.
AC Q9N145;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Names=STAT3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
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```
Matches 192; Conservative 21; Mismatches 15; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDVRRVQDLEQKMKVVENLQDDFDNFYKTLKSQDGM-QDLN 60
Db 130 HPTGTVTEKQMLEHNLQDVRKQVDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDLN 189
QY 61 GNNQ-SVTRQKMQQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLTALDQRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 13
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0003700; F:intracellular signaling cascade; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFE18BEFD8BE CRC64;

Query Match 83.3%; Score 974; DB 2; Length 764;
Best Local Similarity 82.3%; Pred. No. 1.1e-51;
Matches 189; Conservative 21; Mismatches 18; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDVRRVQDLEQKMKVVENLQDDFDNFYKTLKSQDGM-QDLN 60
Db 130 NPSGTVTEKQMLENLQDVRKQVDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDLN 189
QY 61 GNNQ-SVTRQKMQQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLTALDQRRQIVTEMAGLLTAMDYVQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 14
Q13133 PRELIMINARY; PRT; 767 AA.
AC Q13133;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
GN Names=rbStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0003700; F:intracellular signaling cascade; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_Bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match 82.5%; Score 964; DB 2; Length 767;
Best Local Similarity 80.1%; Pred. No. 4.6e-51;
Matches 185; Conservative 25; Mismatches 19; Indels 2; Gaps 2;
QY 1 NHPTAAVTEKQMLEQHLQDVRRVQDLEQKMKVVENLQDDFDNFYKTLKSQDGM-QDL 59
Db 129 SHPSGTVTEKQMLEHNLQDVRKQVDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDM 188
QY 60 GNNQ-SVTRQKMQQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
Db 189 NGNSQAARQKMAQLEQMLTALDQRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 248
QY 119 ETACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 178
Db 249 QIACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 308
QY 179 RIVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 309 KIVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 15
Q9N145 PRELIMINARY; PRT; 163 AA.
AC Q9N145;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Names=STAT3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 121.891 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-30
Perfect score: 1172
Sequence: 1 NPTAAVTEKQMLEQHAQ.....IKTGVQFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq19808:*
2: Geneseq19908:*
3: Geneseq20008:*
4: Geneseq20018:*
5: Geneseq20028:*
6: Geneseq20038:*
7: Geneseq20038b:*
8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1172	100.0	229	4 AAY72862	Aay72862 Mouse Sta
2	1167	99.6	229	4 AAY72850	Aay72850 Mouse Sta
3	1167	99.6	252	4 AAY72846	Aay72846 Mouse Sta
4	1167	99.6	271	4 AAY72841	Aay72841 Mouse Sta
5	1167	99.6	770	2 AAY72082	Aay72082 Mouse Sta
6	1167	99.6	770	2 AAW03176	Aaw03176 Mouse Sta
7	1163	99.2	229	4 AAY72863	Aay72863 Mouse Sta
8	1156	98.6	720	5 AAE22055	Aae22055 Human Sta
9	1156	98.6	769	5 ABB57164	Abb57164 Mouse isc
10	1156	98.6	769	5 AAE22054	Aae22054 Human Sta
11	1156	98.6	769	5 AAE22056	Aae22056 Human pro
12	1156	98.6	770	2 AAR82995	Aar82995 Mouse liv
13	1156	98.6	770	2 AAY03768	Aay03768 Human STA
14	1156	98.6	770	3 AAB12377	Aab12377 N-termina
15	1156	98.6	770	5 AAE14652	Aae14652 Murine ST
16	1156	98.6	770	5 ABG69497	Abg69497 Human bai
17	1156	98.6	770	6 ABU10476	Abu10476 Mouse STA
18	1156	98.6	770	8 ADN04365	Adn04365 Antipeori
19	1156	98.6	770	8 ADP54789	Adp54789 Human PRO
20	1156	98.6	793	3 AAB58442	Aab58442 Lung canc
21	1153	98.4	770	7 ADD44738	Add44738 Rat Prote
22	1152.5	98.3	228	4 AAY72861	Aay72861 Mouse Sta
23	1151	98.2	229	4 AAY72860	Aay72860 Mouse Sta
24	1151	98.2	770	2 AAR82993	Aar82993 Human pia
25	1151	98.2	770	4 AAB19964	Aab19964 Human sig

ALIGNMENTS

RESULT 1

AAY72862
ID AAY72862 standard; protein; 229 AA.
XX AAY72862;
XX AC AAY72862;
XX DT 31-MAY-2001 (first entry)
XX DE Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
XX KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; mutein.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
FT Region 1..25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
FT Misc-difference 19
FT /note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein"
FT Region 213..229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
XX WO200116605-A2.
PD 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX Claim 66; Page 85; 86pp; English.
XX The present sequence is mouse Stat3 mutant (L148A) protein fragment
XX containing 130-358 amino acids of Stat3 protein. This mutant is obtained
CC

26	1151	98.2	770	5	AAE15174	Aae15174 Human Sta
27	1151	98.2	770	7	ADD44740	Add44740 Human Pro
28	1089	92.9	213	4	AAY72851	Aay72851 Mouse Sta
29	1089	92.9	236	4	AAY72847	Aay72847 Mouse Sta
30	1044	89.1	223	4	AAY72854	Aay72854 Mouse Sta
31	845	72.1	185	4	AAY72855	Aay72855 Mouse Sta
32	776	66.2	176	4	AAY72848	Aay72848 Mouse Sta
33	653	55.7	128	4	AAY72852	Aay72852 Mouse Sta
34	600	51.2	143	4	AAY72849	Aay72849 Mouse Sta
35	576	49.1	749	5	AAG78526	Aag78526 Rat STAT-
36	572	48.8	268	4	AAY72844	Aay72844 Mouse Sta
37	572	48.8	582	2	AAW62996	Aaw62996 Human tru
38	572	48.8	582	6	ABU04748	Abu04748 Human exp
39	572	48.8	582	8	ADH57036	Adh57036 Truncated
40	572	48.8	680	6	ABR59713	Abr59713 Human sig
41	572	48.8	712	2	AAR72079	Aar72079 Human Sta
42	572	48.8	712	2	AAW03170	Aaw03170 Human STA
43	572	48.8	712	2	AAW62995	Aaw62995 Human Sta
44	572	48.8	712	6	ABU04747	Abu04747 Human exp
45	572	48.8	712	6	ABU04735	Abu04735 Human exp

CC by replacing Leu 148 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;

Query Match 100.0%; Score 1172; DB 4; Length 229;
 Best Local Similarity 100.0%; Pred. No. 1.2e-101;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEKQOMLEQHAQDVRRKRVQDLQKMKVVENLQDDDFNFKTLKSQGMQDLN 60
 DB 1 NHPTAAVVTKEKQOMLEQHAQDVRRKRVQDLQKMKVVENLQDDDFNFKTLKSQGMQDLN 60
 QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
 DB 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIIKKLELQKVSYGKGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIIKKLELQKVSYGKGDPIVQHRPMLERI 180
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKPEL 229
 DB 181 VELFRNLMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKPEL 229

RESULT 2
 AAY72850
 ID AAY72850 standard; protein; 229 AA.
 XX
 AC AAY72850;
 XX
 DT 31-MAY-2001 (first entry)
 DE
 DE Mouse Stat3 protein fragment #8 (130-358 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.

Key Location/Qualifiers
 Region 1..25
 /note= "Stat3-c-Jun interaction region 1; corresponds to
 130-154 position of Stat3 protein"
 Region 213..229
 /note= "Stat3-c-Jun interaction region 2; corresponds to
 342-358 position of Stat3 protein"

WO200116605-A2.
 XX
 XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JB;
 XX WPI; 2001-226705/23.
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.

XX
 PS
 XX
 CC Claim 65; Page 76-77; 86pp; English.
 CC The present sequence is mouse Stat3 protein fragment containing 130-358
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;

Query Match 99.6%; Score 1167; DB 4; Length 229;
 Best Local Similarity 99.6%; Pred. No. 3.5e-101;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEKQOMLEQHAQDVRRKRVQDLQKMKVVENLQDDDFNFKTLKSQGMQDLN 60
 DB 1 NHPTAAVVTKEKQOMLEQHLQDVRRKRVQDLQKMKVVENLQDDDFNFKTLKSQGMQDLN 60
 QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
 DB 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIIKKLELQKVSYGKGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIIKKLELQKVSYGKGDPIVQHRPMLERI 180
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKPEL 229
 DB 181 VELFRNLMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKPEL 229

RESULT 3
 AAY72846
 ID AAY72846 standard; protein; 252 AA.
 XX
 AC AAY72846;
 XX
 DT 31-MAY-2001 (first entry)
 DE
 DE Mouse Stat3 protein fragment #4 (107-358 amino acids).

Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.

Key Location/Qualifiers
 Region 24..48
 /note= "Stat3-c-Jun interaction region 1; corresponds to
 130-154 position of Stat3 protein"
 Region 236..252
 /note= "Stat3-c-Jun interaction region 2; corresponds to
 342-358 position of Stat3 protein"

WO200116605-A2.
 XX
 XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JB;
 PI

XX DR WPI; 2001-226705/23.
 XX PA Identifying an agent for use in modulating the interaction between
 XX PT transcription factor c-Jun and a Stat3 protein.
 XX PI
 XX PS Claim 65; Page 73; 86pp; English.
 XX XX
 CC The present sequence is mouse Stat3 protein fragment containing 107-358
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX SQ Sequence 252 AA;
 Query Match 99.6%; Score 1167; DB 4; Length 252;
 Best Local Similarity 99.6%; Pred. No. 4e-101;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQKQMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 Db 24 NHPTAAVVTKEQKQMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 83
 QY 61 GNNQSVTRQKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 84 GNNQSVTRQKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
 QY 121 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELQKVKYKGDPIVQHRPMLREI 180
 Db 144 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELQKVKYKGDPIVQHRPMLREI 203
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 204 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKPPPEL 252
 RESULT 4
 AAY72841
 ID AAY72841 standard; protein; 271 AA.
 AC AAY72841;
 XX
 XX 31-MAY-2001 (first entry)
 DT
 DE Mouse Stat3 protein fragment #2 (107-377 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 24..48
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 236..252
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 XX 30-AUG-2000; 2000WO-US023822.
 PF
 XX

PR 31-AUG-1999; 99US-00387418.
 XX
 XX (UVRQ) UNIV ROCKEFELLER.
 XX
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX
 XX Identifying an agent for use in modulating the interaction between
 XX PT transcription factor c-Jun and a Stat3 protein.
 XX PS Claim 65; Page 67-68; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 protein fragment containing 107-377
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX SQ Sequence 271 AA;
 Query Match 99.6%; Score 1167; DB 4; Length 271;
 Best Local Similarity 99.6%; Pred. No. 4.4e-101;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQKQMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 Db 24 NHPTAAVVTKEQKQMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 83
 QY 61 GNNQSVTRQKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 84 GNNQSVTRQKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
 QY 121 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELQKVKYKGDPIVQHRPMLREI 180
 Db 144 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELQKVKYKGDPIVQHRPMLREI 203
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 204 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKPPPEL 252
 RESULT 5
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 AC AAR72082;
 XX
 XX 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX
 XX Mouse Stat3 (19sf6).
 XX
 KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX
 OS Mus sp.
 XX
 PN WO9508629-A1.
 XX
 PD 30-MAR-1995.
 XX
 XX 26-SEP-1994; 94WO-US010849.
 PF
 XX 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126595.

PR 11-MAR-1994; 94US-00212184.
 PR 11-MAR-1994; 94US-00212185.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 XX
 DR WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 XX
 XX Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX
 XX Claim 1; Page 107-110; 160pp; English.
 XX
 CC A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAQ72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 135f1 and 195f6 and encoded proteins termed
 CC Stat4 (AAQ72081) and Stat3 (AAQ72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;
 Query Match 99.6%; Score 1167; DB 2; Length 770;
 Best Local Similarity 99.6%; Pred. No. 1.8e-100;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEOHAQDVRRKRVODLEQKMKVVENLODDFDFNYKTLKSGQDMQDLN 60
 Db 130 NHPTAAVVTKEQOMLEOHLQDVRRKRVODLEQKMKVVENLODDFDFNYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
 QY 121 ACIGGPNICLDRLNWIITSLSAESQLQTRQIQIKLELOQKVSYGKDPVQHRPMLLEERI 180
 Db 250 ACIGGPNICLDRLNWIITSLSAESQLQTRQIQIKLELOQKVSYGKDPVQHRPMLLEERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFTTKVRLLVKRPPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFTTKVRLLVKRPPEL 358
 RESULT 6
 AAQ03176
 ID AAQ03176 standard; protein; 770 AA.
 XX
 AC AAQ03176;
 XX
 XX 24-OCT-1996 (first entry)
 DT
 XX
 DE Mouse STAT4.
 XX
 KW STAT4; signal transducer and activator of transcription;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW autoimmune disease; antagonist; therapy.
 XX
 OS Mus sp.
 XX
 PH Key Location/Qualifiers
 FT Domain
 FT 398...508
 FT /label= DNA binding domain
 FT /note= "Claim 3, page 110"
 FT
 XX
 PN W09620954-A2.
 XX
 XX 11-JUL-1996.

XX 28-DEC-1995; 95WO-US017025.
 XX
 PR 06-JAN-1995; 95US-00369796.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Darnell JE, Wen Z, Horvath CM, Zhong Z;
 XX
 DR WPI; 1996-333941/33.
 DR N-PSDB; AAT31280.
 XX
 XX New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
 PT preventing or treating cellular dysfunction, e.g. oncogenesis,
 PT inflammation, parasitic disease or autoimmunity.
 XX
 XX Disclosure; Page 87-90; 139pp; English.
 XX
 CC Mouse signal transducer and activator of transcription (STAT) protein
 CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
 CC ligand-activated receptor kinase complexes followed by nuclear
 CC translocation and DNA binding to activate transcription. Recombinant
 CC STAT4 can be obt'd. using cDNA clone 195f6 (AAT31278) obt'd. from
 CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
 CC AAQ03167) capable of both receptor recognition and message delivery via
 CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
 CC antagonists used to inhibit STAT-mediated signal transduction and
 CC activation of transcription
 XX
 SQ Sequence 770 AA;
 Query Match 99.6%; Score 1167; DB 2; Length 770;
 Best Local Similarity 99.6%; Pred. No. 1.8e-100;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEOHAQDVRRKRVODLEQKMKVVENLODDFDFNYKTLKSGQDMQDLN 60
 Db 130 NHPTAAVVTKEQOMLEOHLQDVRRKRVODLEQKMKVVENLODDFDFNYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
 QY 121 ACIGGPNICLDRLNWIITSLSAESQLQTRQIQIKLELOQKVSYGKDPVQHRPMLLEERI 180
 Db 250 ACIGGPNICLDRLNWIITSLSAESQLQTRQIQIKLELOQKVSYGKDPVQHRPMLLEERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFTTKVRLLVKRPPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFTTKVRLLVKRPPEL 358
 RESULT 7
 AAQ72863
 ID AAQ72863 standard; protein; 229 AA.
 XX
 AC AAQ72863;
 XX
 XX 31-MAY-2001 (first entry)
 DT
 XX
 DE Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutein.
 XX
 OS Mus musculus.
 XX
 PH Key Location/Qualifiers
 FT Region
 FT 1..25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"

FT Misc-difference 22 /note= "wild type Val substituted with Ala corresponds to
 FT 151 position of Stat-3 protein"
 FT Region 213..229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX WO200116605-A2.
 XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JB;
 XX WPI; 2001-226705/23.
 XX Identifying an agent for use in modulating the interaction between
 XX transcription factor c-Jun and a Stat3 protein.
 XX Claim 66; Page 86; 86pp; English.
 XX The present sequence is mouse Stat3 mutant (V151A) protein fragment
 XX containing 130-358 amino acids of Stat3 protein. This mutant is obtained
 XX by replacing Val 151 with Ala in Stat3 protein. The invention relates to
 XX methods for identifying interacting regions of transcription factors and
 XX methods for identifying agents which modulates the interaction between a
 XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 XX Stat-3, useful for modulating gene transcription e.g., cellular
 XX transformation. These identifying agents are used in the treatment of
 XX dysproliferative diseases and also for treating cancer and psoriasis. A
 XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 XX binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;
 Query Match 99.2%; Score 1163; DB 4; Length 229;
 Best Local Similarity 99.1%; Pred. No. 8.3e-101;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQMLEQHAQDVRKRVQDLERQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 1 NHPTAAVVTKEQMLEQHLQDARKRVQDLERQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 QY 61 GNNQSVTRQKMQLEQMLTALDQNRRSIVSELAGLLSAMYVQKTLTDEBLADWKRRPEI 120
 DB 61 GNNQSVTRQKMQLEQMLTALDQNRRSIVSELAGLLSAMYVQKTLTDEBLADWKRRPEI 120
 QY 121 ACIGGPNICLDRLNWTLSAESOLQTRQOIKKLBELOQKVSXKGDPIVQHRPMLREI 180
 DB 121 ACIGGPNICLDRLNWTLSAESOLQTRQOIKKLBELOQKVSXKGDPIVQHRPMLREI 180
 QY 181 VELFRNLKSAFVVERQPCMPHPDRPLVKTGVQFTKRVLLVKPEL 229
 DB 181 VELFRNLKSAFVVERQPCMPHPDRPLVKTGVQFTKRVLLVKPEL 229
 RESULT 8
 AAE22055
 ID AAE22055 standard; protein; 720 AA.
 XX AC AAE22055;
 XX 25-JUL-2002 (first entry)
 XX Human Stat3beta protein.
 XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW Immune response; Stat3; coronary atherosclerosis; vascular occlusion;

KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.
 XX Homo sapiens.
 XX OS
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 713..714
 FT /note= "Encoded by ACA CCA TTC"
 XX WO200220032-A1.
 XX 14-MAR-2002.
 XX 10-SEP-2001; 2001WO-US028254.
 XX 08-SEP-2000; 2000US-0231212P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX (UYSP-) UNIV SOUTH FLORIDA.
 XX Yu H, Pardoll D, Jove R, Dalton W;
 XX WPI; 2002-362218/39.
 XX N-PSDB; AAD35086.
 XX Modulating angiogenesis and an immune response in an individual, for
 XX treating a hypoxic or ischemic condition, comprises administering a
 XX compound that modulates the activity of a signal transducer and activator
 XX of transcription 3.
 XX
 XX Disclosure; Page 87-89; 94pp; English.
 XX The invention relates to a method of modulating angiogenesis and immune
 XX response. Method involves administering to an individual a compound that
 XX modulate the activity of signal transducer and activator of transcription
 XX 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 XX hypoxic or ischaemic condition or disorder which is the result of stroke,
 XX ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 XX tissue ischaemia in the lower extremities, infarction, trauma, vascular
 XX occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 XX chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 XX epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 XX nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 XX with neovascularisation. Suppressing an immune response is useful for
 XX ameliorating a symptom of an autoimmune disease such as systemic lupus
 XX erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 XX Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 XX mixed connective tissue disease, primary biliary cirrhosis, pernicious
 XX anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 XX gluten-sensitive enteropathy, autoimmune neuropenia, myasthenia gravis,
 XX idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 XX disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 XX infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 XX dense deposit disease. The method is useful in preventing or treating
 XX specific proliferative and oncogenic disease which includes sarcomas and
 XX carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 XX fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 XX hypoproliferative disorders, physical trauma, lesions and wounds. The
 XX method is also used in gene therapy. The present sequence is human
 XX Stat3beta protein
 XX
 SQ Sequence 720 AA;

Query Match 98.6%; Score 1156; DB 5; Length 720;
 Best Local Similarity 98.7%; Pred. No. 1.8e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVKRKYQDLEQKMKVVENIQDDPDFNFKTLKSQGDMDQDLN 60
 |||||
 Db 130 NHPTAAVTEKQOMLEQHLQDVKRKYQDLEQKMKVVENIQDDPDFNFKTLKSQGDMDQDLN 189
 |||||
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 |||||
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI 249
 |||||
 QY 121 ACIGGPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSYGKDPVQHRPMLERI 180
 |||||
 Db 250 ACIGGPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSYGKDPVQHRPMLERI 309
 |||||
 QY 181 VELFRNLMSAFVVERQPCMPMHPDRPLVKTGVQFTTKVRLLVKPEL 229
 |||||
 Db 310 VELFRNLMSAFVVERQPCMPMHPDRPLVKTGVQFTTKVRLLVKPEL 358
 |||||

RESULT 9

ABBS57164
 ID ABB57164 standard; protein; 769 AA.

XX ABB57164;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related protein sequence SEQ ID NO:398.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX Mus musculus.

XX W0200188188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP004192.

XX 18-MAY-2000; 2000JP-00145977.

XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

XX N-PSDB; AB199454.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.

XX Claim 2; Page 1084-1087; 2690pp; English.

XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention

XX Sequence 769 AA;

SQ

Query Match 98.6%; Score 1156; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 1.9e-99;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVKRKYQDLEQKMKVVENIQDDPDFNFKTLKSQGDMDQDLN 60
 |||||
 Db 130 NHPTAAVTEKQOMLEQHLQDVKRKYQDLEQKMKVVENIQDDPDFNFKTLKSQGDMDQDLN 189
 |||||
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 |||||
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI 249
 |||||
 QY 121 ACIGGPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSYGKDPVQHRPMLERI 180
 |||||
 Db 250 ACIGGPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSYGKDPVQHRPMLERI 309
 |||||
 QY 181 VELFRNLMSAFVVERQPCMPMHPDRPLVKTGVQFTTKVRLLVKPEL 229
 |||||
 Db 310 VELFRNLMSAFVVERQPCMPMHPDRPLVKTGVQFTTKVRLLVKPEL 358
 |||||

RESULT 10

AAE22054

ID AAE22054 standard; protein; 769 AA.

XX AAE22054;

XX 25-JUL-2002 (first entry)

XX Human Stat3 protein.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

XX Homo sapiens.

XX W0200220032-A1.

XX 14-MAR-2002.

XX 10-SEP-2001; 2001WO-US028254.

XX 08-SEP-2000; 2000US-0231212P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Yu H, Pardoll D, Jove R, Dalton W;

XX WPI; 2002-362218/39.

XX N-PSDB; AAD35065.

XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.

XX Disclosure; Page 83-85; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing

CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neuropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein
 CC
 XX
 SQ Sequence 769 AA;

Query Match 98.6%; Score 1156; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 1.9e-99;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFNYTKLSQGDMDLN 60
 Db 130 NHPTAAVVTKEQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDDFNYTKLSQGDMDLN 189
 QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
 Db 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 249
 QY 121 ACIGGPPNICDLRLENWITSLSAQLOTRQIKKLELOQKVS YKGDPIVQHRPMLERI 180
 Db 250 ACIGGPPNICDLRLENWITSLSAQLOTRQIKKLELOQKVS YKGDPIVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
 Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 358

RESULT 11

AAE22056
 ID AAE22056 standard; protein; 769 AA.

AC AAE22056;

XX 25-JUL-2002 (first entry)

DE Human protein related to angiogenesis regulation.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

XX Homo sapiens.

XX

PN

WO200220032-A1.

XX

14-MAR-2002.

PD

10-SEP-2001; 2001WO-US028254.

XX

08-SEP-2000; 2000US-0231212P.

PR

(UYJO) UNIV JOHNS HOPKINS.
 (UYSF-) UNIV SOUTH FLORIDA.

XX

Yu H, Pardoll D, Jove R, Dalton W;

XX

WPI; 2002-362218/39.

DR

Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.

XX

Disclosure; Page 83-85; 94pp; English.

XX

The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neuropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation

XX Sequence 769 AA;

Query Match 98.6%; Score 1156; DB 5; Length 769;

Best Local Similarity 98.7%; Pred. No. 1.9e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY

1 NHPTAAVVTKEQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFNYTKLSQGDMDLN 60

Db

130 NHPTAAVVTKEQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDDFNYTKLSQGDMDLN 189

QY

61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120

Db

190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 249

QY

121 ACIGGPPNICDLRLENWITSLSAQLOTRQIKKLELOQKVS YKGDPIVQHRPMLERI 180

Db

250 ACIGGPPNICDLRLENWITSLSAQLOTRQIKKLELOQKVS YKGDPIVQHRPMLERI 309

QY

181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229

Db

310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 358

RESULT 12

AAR82995
ID AAR82995 standard; protein; 770 AA.

XX
AC AAR82995;

XX
DT 25-MAR-1996 (first entry)

XX
DE Mouse liver acute phase response factor.

XX
KW Mouse; acute phase response factor; transcription factor; interleukin-6;
KW signal transmission; liver; antibody; antisense; ribozyme;
KW antiinflammatory; antitumor; hypotensive; therapy.

XX
OS Mus musculus.

XX
PN EP676469-A2.

XX
PD 11-OCT-1995.

XX
PF 29-MAR-1995; 95EP-00104670.

XX
PR 04-APR-1994; 94JP-00065825.

XX
PA (KISH/) KISHIMOTO T.

XX
PI Akira S, Kishimoto T;

XX
DR WPI; 1995-346089/45.

XX
DR N-PSDB; AAT05619.

XX
PT New acute phase response factor - for developing inhibitory agents for
PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
PT diseases.

XX
PS Claim 10; Page 20-22; 31pp; English.

XX
CC The sequence represents a mouse acute phase response factor (APRF), a
CC transcription factor related to signal transmission of interleukin-6 (IL-
CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
CC library using a polymerase chain reaction product (amplified using
CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
CC inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
CC hypertension, etc

XX
SQ Sequence 770 AA;

Query Match 98.6%; Score 1156; DB 2; Length 770;

Best Local Similarity 98.7%; Pred. No. 1.9e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60

DB 130 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

DB 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGGPPNICLDRLNNITSLAESOLQTRQOIKKLELQKQVSKGDPPIVQHRPMLERI 180

DB 250 ACIGGPPNICLDRLNNITSLAESOLQTRQOIKKLELQKQVSKGDPPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 13

AAY03768

ID AAY03768 standard; protein; 770 AA.

XX
AC AAY03768;

XX
DT 11-JUN-1999 (first entry)

XX
DE Human STAT3 allelic variant.

XX
KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
KW intracellular transcription factor; interleukin-6; medicament; variant;
KW pharmaceutical; autoimmune disease; inflammatory; human.

XX
OS Homo sapiens.

XX
PN EP905234-A2.

XX
PD 31-MAR-1999.

XX
PF 18-FEB-1998; 98EP-00102774.

XX
PR 16-SEP-1997; 97EP-00116061.

XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX
PI Serlupi-Crescenzi O, Della Pietra L;

XX
DR WPI; 1999-192664/17.

XX
DR N-PSDB; AAY29281.

XX
PT New human Signal Transducer and Activator of Transcription 3 (STAT3)
PT allelic variant useful for treatment of autoimmune and inflammatory
PT disease.

XX
PS Claim 2; Page 9-13; 32pp; English.

XX
CC The present sequence represents a predominant allelic variant of human
CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
CC intracellular transcription factor which mediates IL-6 signals. The
CC encoding sequence differs from the original published human STAT3 gene
CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
CC DNA molecule can be used for the recombinant expression of the variant.
CC STAT3 protein is useful as a medicament or pharmaceutical composition for
CC treatment of autoimmune or inflammatory diseases

XX
SQ Sequence 770 AA;

Query Match 98.6%; Score 1156; DB 2; Length 770;

Best Local Similarity 98.7%; Pred. No. 1.9e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60

DB 130 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

DB 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGGPPNICLDRLNNITSLAESOLQTRQOIKKLELQKQVSKGDPPIVQHRPMLERI 180

DB 250 ACIGGPPNICLDRLNNITSLAESOLQTRQOIKKLELQKQVSKGDPPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

08-NOV-2000 (first entry)

N-terminal domain of murine STAT-3 protein.

STAT; signal transducer and activator of transcription; crystal; drug design; murine.

Mus sp.

Key Location/Qualifiers

Region 4..9

FT /label= Alpha helix 1

Region 12..21

FT /label= Alpha helix 2

Region 19..21

FT /label= 3(10) helix of alpha helix 2

Region 28..33

FT /label= Alpha helix 3

Region 35..40

FT /label= Alpha helix 4

Region 43..47

FT /label= Alpha helix 5

Region 50..73

FT /label= Alpha helix 6

Region 77..96

FT /label= Alpha helix 7

Region 99..119

FT /label= Alpha helix 8

XX US6087478-A.

XX 11-JUL-2000.

XX 23-JAN-1998; 98US-00012710.

XX 23-JAN-1998; 98US-00012710.

XX (UYRQ) UNIV ROCKEFELLER.

XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;

XX WPI; 2000-505108/45.

XX New crystals of an N-terminal fragment of a signal transducer and

XX activator of transcription that effectively diffracts x-rays, useful for

XX drug screening and development.

XX Disclosure; Fig 1; 42pp; English.

XX The present invention relates to a crystal of an N-terminal fragment of a

XX signal transducer and activator of transcription (STAT) protein. The

XX crystal effectively diffracts x-rays, allowing the determination of the

XX atomic coordinates of the N-terminal domain to a resolution of greater

XX than 5.0 Angstroms. The present sequence is the N-terminal domain of the

XX murine STAT 3 protein. The N-terminal domain enables STAT dimers to

XX interact and bind DNA cooperatively, a mechanism important for gene

XX activation. The crystals are useful in drug screening and development by

XX selecting a potential drug by performing rational drug design with the 3-

XX dimensional structure determined for the crystal

XX Sequence 770 AA;

Query Match 98.6%; Score 1156; DB 3; Length 770;

Best Local Similarity 98.7%; Pred. No. 1.9e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLSEHAQVVRKRVQDLQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60

DB 130 NHPTAAVTEKQMLSEHAQVVRKRVQDLQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 120

DB 190 GNNQSVTRQKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRQOI 249

QY 121 ACIGGPNICLDRLNWNITSLAESQLQTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180

DB 250 ACIGGPNICLDRLNWNITSLAESQLQTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVITKGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPDRPLVITKGVQFTTKVRLLVKFPPEL 358

RESULT 15

AAE14652

ID AAE14652 standard; protein; 770 AA.

XX AAE14652;

XX 16-JUL-2002 (first entry)

XX Murine STAT3 protein.

XX Signal transducer and activator of transcription; STAT3;

XX drug development; drug discovery; crystal; inflammation; allergy; asthma;

XX leukemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity;

XX viral disease; growth retardation; murine.

XX Mus sp.

XX Key Location/Qualifiers

FT Domain 1..130

FT /note= "Conserved N-terminal domain of the STAT family"

XX US6312887-B1.

XX 06-NOV-2001.

XX 24-APR-2000; 2000US-00556273.

XX 23-JAN-1998; 98US-00012710.

XX (UYRQ) UNIV ROCKEFELLER.

XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;

XX WPI; 2002-033337/04.

XX Identifying compounds that bind to signal transducer and activator of

XX transcription proteins, useful for the production of new drugs.

XX Example; Col 47-50; 44pp; English.

XX The invention relates to methods for detecting compounds that bind to

XX signal transducer and activator of transcription (STAT) proteins for the

XX discovery and development of new drug compounds based on the structural

XX properties of the protein crystal. The methods include: identifying a

XX compound that binds to the N-terminal domain of a STAT protein,

XX identifying a compound that enhances or diminishes the binding of the

XX dimeric STAT proteins to each other and/or their nucleic acid binding

XX site; or identifying a compound that enhances or diminishes the ability

XX of STAT protein dimers to induce the expression of a gene operably under

XX the control of a promoter containing at least two adjacent weak binding

XX sites for STAT protein dimers. The methods are used for identifying new

XX drugs. An antagonist of STAT N-terminal dimeric interactions that

XX inhibits the binding of the STAT dimers to adjacent weak binding sites on

XX a promoter of a gene, could be useful as drugs in the treatment of

XX diseases, e.g. inflammation, allergy, asthma and leukaemia. On the other

XX hand, an agonist of N-terminal dimeric interactions between STAT dimers,

XX can be used as drugs in the treatment of diseases e.g. anaemia,

XX neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and

XX growth retardation. The present sequence is murine STAT3 protein

XX Sequence 770 AA;

Query Match

98.6%; Score 1156; DB 5; Length 770;

Best Local Similarity 98.7%; Pred. NO. 1.9e-99;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	NHPTAAVTEKQOMLEQHAQDVKRVQDLEOKMKVVENLQDDPFDNYKTKSQGDMODLN	60
Db	130	NHPTAAVTEKQOMLEQHLQDVKRVQDLEOKMKVVENLQDDPFDNYKTKSQGDMODLN	189
QY	61	GNNQSVTRQKMQOLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI	120
Db	190	GNNQSVTRQKMQOLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI	249
QY	121	ACIGGPPNICLDRLNWTSLAESQLQTRQIQIKKLEELQOKVSYKGDPIVQHRPMLEERI	180
Db	250	ACIGGPPNICLDRLNWTSLAESQLQTRQIQIKKLEELQOKVSYKGDPIVQHRPMLEERI	309
QY	181	VELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL	229
Db	310	VELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL	358

Search completed: May 25, 2005, 17:36:38
Job time : 123.057 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 28.6534 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-30
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHAQ.....IKTGVQFTTKVRLLVKPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1172	100.0	229	3	US-09-387-418A-30
2	1167	99.6	229	3	US-09-387-418A-18
3	1167	99.6	229	3	US-09-387-418A-28
4	1167	99.6	252	3	US-09-387-418A-14
5	1167	99.6	271	3	US-09-387-418A-9
6	1167	99.6	770	1	US-08-369-796-12
7	1167	99.6	770	2	US-08-852-091-12
8	1167	99.6	770	2	US-08-820-754-12
9	1167	99.6	770	3	US-08-956-652-12
10	1167	99.6	770	3	US-08-956-869-12
11	1167	99.6	770	3	US-08-948-547-12
12	1167	99.6	770	3	US-09-364-970-3
13	1167	99.6	770	3	US-09-364-970-5
14	1167	99.6	770	3	US-08-956-653A-12
15	1167	99.6	770	4	US-08-212-185-12
16	1167	99.6	770	5	PCT-US95-17025-12
17	1163	99.2	229	3	US-09-387-418A-31
18	1156	98.6	770	1	US-08-416-581B-9
19	1156	98.6	770	3	US-09-012-710-8
20	1156	98.6	770	3	US-09-556-273-8
21	1156	98.6	770	3	US-09-526-542-2
22	1156	98.6	770	4	US-10-117-087-2
23	1151	98.2	770	1	US-08-416-581B-1
24	1151	98.2	770	1	US-08-416-581B-5
25	1151	98.2	770	3	US-09-087-465-6
26	1151	98.2	770	4	US-09-972-800A-6
27	1151	98.2	771	1	US-08-276-099A-14

28	1151	98.2	771	1	US-08-781-890-14	Sequence 14, Appl
29	1150	98.1	229	3	US-09-387-418A-29	Sequence 29, Appl
30	1089	92.9	213	3	US-09-387-418A-19	Sequence 19, Appl
31	1089	92.9	236	3	US-09-387-418A-15	Sequence 15, Appl
32	1044	89.1	223	3	US-09-387-418A-22	Sequence 22, Appl
33	845	72.1	185	3	US-09-387-418A-23	Sequence 23, Appl
34	776	66.2	176	3	US-09-387-418A-16	Sequence 16, Appl
35	653	55.7	128	3	US-09-387-418A-20	Sequence 20, Appl
36	600	51.2	143	3	US-09-387-418A-17	Sequence 17, Appl
37	572	48.8	268	3	US-09-387-418A-12	Sequence 12, Appl
38	572	48.8	582	4	US-09-430-806A-3	Sequence 3, Appl
39	572	48.8	712	1	US-08-369-796-6	Sequence 6, Appl
40	572	48.8	712	2	US-08-852-091-6	Sequence 6, Appl
41	572	48.8	712	2	US-08-820-754-6	Sequence 6, Appl
42	572	48.8	712	3	US-08-956-652-6	Sequence 6, Appl
43	572	48.8	712	3	US-08-956-869-6	Sequence 6, Appl
44	572	48.8	712	3	US-08-948-547-6	Sequence 6, Appl
45	572	48.8	712	3	US-08-956-653A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-387-418A-30
; Sequence 30, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzreszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-387-418A-30

Query Match	100.0%;	Score 1172;	DB 3;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 1e-97;		
Matches 229;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDDFDNFKTLKSGQDMQDLN	60	
Db	1	NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDDFDNFKTLKSGQDMQDLN	60	
QY	61	GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI	120	
Db	61	GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI	120	
QY	121	ACIGGPNICLDRLENNITSLAESQLQTRQIKKLELOKQVSKGDPVQHRPMLERI	180	
Db	121	ACIGGPNICLDRLENNITSLAESQLQTRQIKKLELOKQVSKGDPVQHRPMLERI	180	
QY	181	VELFRNLMSAFVVERQPCWMPHDPRLVIKTGVQFTTKVRLLVKPEL	229	
Db	181	VELFRNLMSAFVVERQPCWMPHDPRLVIKTGVQFTTKVRLLVKPEL	229	

RESULT 2

US-09-387-418A-18
; Sequence 18, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzreszczynska, Melissa H

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; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-18

Query Match      99.6%; Score 1167; DB 3; Length 229;
Best Local Similarity 99.6%; Pred. No. 2.9e-97;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFKTLKSGQDMQDLN 60
DB 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFKTLKSGQDMQDLN 60
QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
QY 121 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 180
DB 121 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 180
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 3
US-09-387-418A-28
; Sequence 28, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-28

Query Match      99.6%; Score 1167; DB 3; Length 229;
Best Local Similarity 99.6%; Pred. No. 2.9e-97;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFKTLKSGQDMQDLN 60
DB 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFKTLKSGQDMQDLN 60
QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
QY 121 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 180
DB 121 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 180
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 4
US-09-387-418A-14
; Sequence 14, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-14

Query Match      99.6%; Score 1167; DB 3; Length 252;
Best Local Similarity 99.6%; Pred. No. 3.3e-97;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFKTLKSGQDMQDLN 60
DB 24 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFKTLKSGQDMQDLN 83
QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
QY 121 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 180
DB 144 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 203
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
DB 204 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 252

RESULT 5
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match      99.6%; Score 1167; DB 3; Length 271;
Best Local Similarity 99.6%; Pred. No. 3.6e-97;

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QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 4
US-09-387-418A-14
; Sequence 14, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-14

Query Match      99.6%; Score 1167; DB 3; Length 252;
Best Local Similarity 99.6%; Pred. No. 3.3e-97;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFKTLKSGQDMQDLN 60
DB 24 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFKTLKSGQDMQDLN 83
QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
QY 121 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 180
DB 144 ACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 203
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
DB 204 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 252

RESULT 5
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match      99.6%; Score 1167; DB 3; Length 271;
Best Local Similarity 99.6%; Pred. No. 3.6e-97;

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Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQADVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
DB 24 NHPTAAVTEKQOMLEQHLQADVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 83
QY 61 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 84 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
QY 121 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLEREI 180
DB 144 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLEREI 203
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPEL 229
DB 204 VELFRNLMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPEL 252

RESULT 6
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-369-796-12

Query Match 99.6%; Score 1167; DB 1; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQADVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQADVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 84 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
QY 121 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLEREI 180
DB 144 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLEREI 203
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPEL 229
DB 204 VELFRNLMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPEL 252

DB 190 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLEREI 180
DB 250 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLEREI 309
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPEL 229
DB 310 VELFRNLMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKPEL 358

RESULT 7
US-08-852-091-12
; Sequence 12, Application US/08852091
; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-852-091-12

Query Match 99.6%; Score 1167; DB 2; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQADVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQADVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLEREI 180
DB 250 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLEREI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 358

RESULT 8
 US-08-754-12
 ; Sequence 12, Application US/08820754
 ; Patent No. 5976835
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zilong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/820,754
 ; FILING DATE: 19-MAR-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-754-12

Query Match 99.6%; Score 1167; DB 2; Length 770;
 Best Local Similarity 99.6%; Pred. No. 1.4e-96;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQADVRKQVQDLEQKMKVVENLODDFNFYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVVTKEQOMLEQADVRKQVQDLEQKMKVVENLODDFNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQLEQMLTALDQRRSIVSELAGLSAMEYVQKTLTDEELADWKRRPEI 120
 DB 190 GNNQSVTRQKMQLEQMLTALDQRRSIVSELAGLSAMEYVQKTLTDEELADWKRRPEI 249
 QY 121 ACIGGPNICLDRLNWTSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
 DB 250 ACIGGPNICLDRLNWTSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 358

RESULT 9
 US-08-956-652-12
 ; Sequence 12, Application US/08956652
 ; Patent No. 6013475
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zilong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/956,652
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-956-652-12

Query Match 99.6%; Score 1167; DB 3; Length 770;


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Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVVENLQDDPFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVVENLQDDPFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQMKOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQMKOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDRLENWITSLSAESQLQTRQOIKKLEELQKVSQKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLENWITSLSAESQLQTRQOIKKLEELQKVSQKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLPVIKTGQVQFTTKVRLLVKFPPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLPVIKTGQVQFTTKVRLLVKFPPEL 358

RESULT 10
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELETYPE: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVVENLQDDPFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVVENLQDDPFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQMKOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQMKOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDRLENWITSLSAESQLQTRQOIKKLEELQKVSQKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLENWITSLSAESQLQTRQOIKKLEELQKVSQKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLPVIKTGQVQFTTKVRLLVKFPPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLPVIKTGQVQFTTKVRLLVKFPPEL 358

RESULT 11
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELGILLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELGILLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGPPNICLDRLNNWITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLNNWITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 12
US-09-364-970-3
Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-3

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELGILLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELGILLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGPPNICLDRLNNWITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLNNWITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 13
US-09-364-970-5
Sequence 5, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-5

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELGILLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELGILLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGPPNICLDRLNNWITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLNNWITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 14
US-08-956-653A-12
Sequence 12, Application US/08956653A
Patent No. 6338949
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994

APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-956-653A-12

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNYKTLKSQGMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDRLENWITSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLENWITSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 358

RESULT 15
US-08-212-185-12
Sequence 12, Application US/08212185
Patent No. 6605442
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James B.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-212-185-12

Query Match 99.6%; Score 1167; DB 4; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNYKTLKSQGMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDRLENWITSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLENWITSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 358

Search completed: May 25, 2005, 17:47:40
Job time : 29.6534 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:36:58 ; Search time 100.287 Seconds
(without alignments)
763.830 Million cell updates/sec

Title: US-10-090-185-30
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQMLEQHAQ.....IKTGVOFTKRVLLVFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1167	99.6	229	13	US-10-090-185-18
3	1167	99.6	229	13	US-10-090-185-28
4	1167	99.6	252	13	US-10-090-185-14
5	1167	99.6	271	13	US-10-090-185-9
6	1167	99.6	770	11	US-09-876-773-12
7	1167	99.6	770	17	US-10-639-617-11
8	1163	99.2	229	13	US-10-090-185-31
9	1156	98.6	720	15	US-10-380-020-4
10	1156	98.6	769	15	US-10-380-020-2
11	1156	98.6	769	15	US-10-380-020-5
12	1156	98.6	770	14	US-10-045-792-8
13	1156	98.6	770	14	US-10-038-010-56

14	1156	98.6	770	14	US-10-117-087-2	Sequence 2, Appli
15	1156	98.6	793	9	US-09-925-302-780	Sequence 780, App
16	1156	98.6	793	10	US-09-925-302-780	Sequence 780, App
17	1153	98.4	770	15	US-10-116-275-329	Sequence 329, App
18	1151	98.2	770	15	US-10-116-275-349	Sequence 349, App
19	1150	98.1	229	13	US-10-090-185-29	Sequence 29, Appl
20	1089	92.9	213	13	US-10-090-185-19	Sequence 19, Appl
21	1089	92.9	236	13	US-10-090-185-15	Sequence 15, Appl
22	1044	89.1	223	13	US-10-090-185-22	Sequence 22, Appl
23	845	72.1	185	13	US-10-090-185-23	Sequence 23, Appl
24	776	66.2	176	13	US-10-090-185-16	Sequence 16, Appl
25	653	55.7	128	13	US-10-090-185-20	Sequence 20, Appl
26	600	51.2	143	13	US-10-090-185-17	Sequence 17, Appl
27	576	49.1	749	9	US-09-833-205-4	Sequence 4, Appli
28	572	48.8	268	13	US-10-090-185-12	Sequence 12, Appl
29	572	48.8	582	14	US-10-245-120-3	Sequence 3, Appli
30	572	48.8	712	11	US-09-876-773-6	Sequence 6, Appli
31	572	48.8	712	14	US-10-245-120-2	Sequence 2, Appli
32	572	48.8	712	17	US-10-639-617-6	Sequence 6, Appli
33	572	48.8	712	17	US-10-936-390-5	Sequence 2, Appli
34	572	48.8	750	9	US-09-833-205-2	Sequence 4, Appli
35	572	48.8	750	11	US-09-876-773-4	Sequence 1, Appli
36	572	48.8	750	14	US-10-245-120-1	Sequence 1, Appli
37	572	48.8	750	14	US-10-308-279-44	Sequence 44, Appl
38	572	48.8	750	16	US-10-755-889-352	Sequence 352, App
39	572	48.8	750	16	US-10-755-889-823	Sequence 823, App
40	572	48.8	750	17	US-10-492-043-19	Sequence 19, Appl
41	572	48.8	750	17	US-10-639-617-4	Sequence 4, Appli
42	572	48.8	786	9	US-09-925-297-550	Sequence 550, App
43	571	48.7	129	13	US-10-090-185-24	Sequence 24, Appl
44	565	48.2	749	9	US-09-833-205-6	Sequence 6, Appli
45	565	48.2	749	11	US-09-876-773-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-30

Query Match 100.0%; Score 1172; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.3e-95;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NHPTAAVTEKQMLEQHAQDVQRKRVQDLEQRKVVENLODDPFDNYKTLKSGQMDQDLN 60
Db 1 NHPTAAVTEKQMLEQHAQDVQRKRVQDLEQRKVVENLODDPFDNYKTLKSGQMDQDLN 60
Qy 61 GNNQSVTRKMOQLEQMLTALDQMRRSIVSELAGLLSMEYYQKTLTDBELADWKRREI 120
Db 61 GNNQSVTRKMOQLEQMLTALDQMRRSIVSELAGLLSMEYYQKTLTDBELADWKRREI 120

Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 2
US-10-090-185-18
; Sequence 18, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-18

Query Match 99.6%; Score 1167; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 60
Db 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 60
Qy 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 3
US-10-090-185-28
; Sequence 28, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28

; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-28

Query Match 99.6%; Score 1167; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 60
Db 1 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 60
Qy 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 4
US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 99.6%; Score 1167; DB 13; Length 252;
Best Local Similarity 99.6%; Pred. No. 7.2e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 60
Db 24 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 83
Qy 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 84 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Db 144 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 203
Qy 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 204 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 252

RESULT 5
US-10-090-185-9

; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-9

Query Match 99.6%; Score 1167; DB 13; Length 271;
Best Local Similarity 99.6%; Pred. No. 7.9e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
Db 24 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 83
QY 61 GNNQSVTRKQMOLEQMLTALDOMRBSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 120
Db 84 GNNQSVTRKQMOLEQMLTALDOMRBSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 143
QY 121 ACIGGPPNICLDRLNENWITSLAESQLQTRQIQIKLEELQKVKYKGDPIVQHRPMLERI 180
Db 144 ACIGGPPNICLDRLNENWITSLAESQLQTRQIQIKLEELQKVKYKGDPIVQHRPMLERI 203
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
Db 204 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 252

RESULT 6
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 343-5800
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 99.6%; Score 1167; DB 11; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
Db 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 189
QY 61 GNNQSVTRKQMOLEQMLTALDOMRBSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRKQMOLEQMLTALDOMRBSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDRLNENWITSLAESQLQTRQIQIKLEELQKVKYKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLNENWITSLAESQLQTRQIQIKLEELQKVKYKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 7
US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/639,617
 ; FILING DATE: 12-AUG-2003
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELE: 133521

; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 US-10-639-617-12

Query Match 99.6%; Score 1167; DB 17; Length 770;
 Best Local Similarity 99.6%; Pred. No. 3e-94;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVODLEQKMKVVENLODDDFNFKTLKSGQDMODLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVODLEQKMKVVENLODDDFNFKTLKSGQDMODLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 190 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
 QY 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
 DB 250 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 8
 US-10-090-185-31
 ; Sequence 31, Application US/10090185
 ; Publication No. US20020197647A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Xiaokui
 ; APPLICANT: Wzreszczyńska, Melissa H
 ; APPLICANT: Horvath, Curt M
 ; APPLICANT: Darnell Jr., James E
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
 ; TITLE OF INVENTION: INTERACTIONS
 ; FILE REFERENCE: 600-1-253
 ; CURRENT APPLICATION NUMBER: US/10/090,185
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: 09/387,418
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 31
 ; LENGTH: 229

; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-090-185-31
 Query Match 99.2%; Score 1163; DB 13; Length 229;
 Best Local Similarity 99.1%; Pred. No. 1.4e-94;
 Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVODLEQKMKVVENLODDDFNFKTLKSGQDMODLN 60
 DB 1 NHPTAAVTEKQOMLEQHLQDVVRKRVODLEQKMKVVENLODDDFNFKTLKSGQDMODLN 60
 QY 61 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 61 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 QY 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
 DB 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

RESULT 9
 US-10-380-020-4
 ; Sequence 4, Application US/10380020
 ; Publication No. US20040052762A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Hua
 ; APPLICANT: Pardoll, Drew
 ; APPLICANT: Jove, Richard
 ; APPLICANT: Dalton, William
 ; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
 ; FILE REFERENCE: 10873-009-999
 ; CURRENT APPLICATION NUMBER: US/10/380,020
 ; CURRENT FILING DATE: 2003-03-07
 ; PRIOR APPLICATION NUMBER: 60/231,212
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 720
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-380-020-4

Query Match 98.6%; Score 1156; DB 15; Length 720;
 Best Local Similarity 98.7%; Pred. No. 2.6e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVODLEQKMKVVENLODDDFNFKTLKSGQDMODLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVODLEQKMKVVENLODDDFNFKTLKSGQDMODLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 190 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
 QY 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
 DB 250 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 10
 US-10-380-020-2
 ; Sequence 2, Application US/10380020
 ; Publication No. US20040052762A1

GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Fardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match 98.6%; Score 1156; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.8e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLELOQKVSYGKDPVQHRPMLERI 180
DB 250 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLELOQKVSYGKDPVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVKTGQVQTTKVRLLVKEPEL 229
DB 310 VELFRNLMSAFVVERQPCMPHPDRPLVKTGQVQTTKVRLLVKEPEL 358

RESULT 11
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Fardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match 98.6%; Score 1156; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.8e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

DB 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLELOQKVSYGKDPVQHRPMLERI 180
DB 250 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLELOQKVSYGKDPVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVKTGQVQTTKVRLLVKEPEL 229
DB 310 VELFRNLMSAFVVERQPCMPHPDRPLVKTGQVQTTKVRLLVKEPEL 358

RESULT 12
US-10-045-792-8
; Sequence 8, Application US/10045792
; Publication No. US20030003563A1
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; Moarefi, Ismail
; Darnell, Jr., James E.
; Kuriyan, John

TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-045-792-8
Query Match 98.6%; Score 1156; DB 14; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.9e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKSVYKGDPIVQHRPMLERI 309
 Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 13

US-10-038-010-56
 ; Sequence 56, Application US/10038010
 ; Publication No. US20030040089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYBRIGENICS
 ; APPLICANT: Pierre, Legrain
 ; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
 ; FILE REFERENCE: B4767A
 ; CURRENT APPLICATION NUMBER: US/10/038,010
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 60/259,377
 ; PRIOR FILING DATE: 2001-01-02
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 56
 ; LENGTH: 770
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: STAT3 : Transcription factor
 ; LOCATION: (1)..(770)
 ; OTHER INFORMATION:
 US-10-038-010-56

Query Match 98.6%; Score 1156; DB 14; Length 770;
 Best Local Similarity 98.7%; Pred. No. 2.9e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLODDPFDNFYKTLKSQGDMDLN 60
 Db 130 NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLODDPFDNFYKTLKSQGDMDLN 189
 Qy 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
 Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKSVYKGDPIVQHRPMLERI 309
 Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 14

US-10-117-087-2
 ; Sequence 2, Application US/10117087
 ; Publication No. US20030166854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SERLUPI-CRESCENZI, Ottaviano
 ; APPLICANT: DELLA PIETRA, Linda
 ; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
 ; FILE REFERENCE: SERLUPI-2
 ; CURRENT APPLICATION NUMBER: US/10/117,087
 ; CURRENT FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: US/09/526,542
 ; PRIOR FILING DATE: 2000-03-19
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 770
 ; TYPE: PRT

; ORGANISM: Human
 US-10-117-087-2
 Query Match 98.6%; Score 1156; DB 14; Length 770;
 Best Local Similarity 98.7%; Pred. No. 2.9e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLODDPFDNFYKTLKSQGDMDLN 60
 Db 130 NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLODDPFDNFYKTLKSQGDMDLN 189
 Qy 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
 Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKSVYKGDPIVQHRPMLERI 309
 Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 15

US-09-925-302-780
 ; Sequence 780, Application US/09925302
 ; Patent No. US20020044941A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA104
 ; CURRENT APPLICATION NUMBER: US/09/925,302
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05918
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 896
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 780
 ; LENGTH: 793
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-302-780

Query Match 98.6%; Score 1156; DB 9; Length 793;
 Best Local Similarity 98.7%; Pred. No. 3e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLODDPFDNFYKTLKSQGDMDLN 60
 Db 153 NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLODDPFDNFYKTLKSQGDMDLN 212
 Qy 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 213 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 272
 Qy 121 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKSVYKGDPIVQHRPMLERI 180
 Db 273 ACIGPPNICLDRLNWTSLAESQLOTRQOIKKLELOQKSVYKGDPIVQHRPMLERI 332
 Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 333 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 381

Search completed: May 25, 2005, 18:21:54
 Job time : 101.62 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-30
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEBQHAQ.....IKTGVOFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1156	98.6	770	2 I49508	ISGF3 p91-related
2	1151	98.2	770	2 A54444	DNA-binding protei
3	526.5	44.9	739	2 A46159	interferon-depende
4	511	43.6	748	2 A56047	gamma-interferon a
5	321	27.4	851	2 A46160	interferon alpha-1
6	268.5	22.9	786	2 I49274	mammary gland fact
7	268.5	22.9	793	2 S54772	mammary gland fact
8	262.5	22.4	794	2 G02317	transcription acti
9	237	20.2	794	2 S55527	mammary gland fact
10	124.5	10.6	848	2 A54740	interleukin-4 indu
11	121	10.3	978	2 A70387	conserved hypotet
12	119.5	10.2	837	2 I57557	DNA-Binding Protei
13	119.5	10.2	2094	2 S33124	tpc protein - huma
14	119	10.2	533	2 G72593	hypothetical prote
15	118.5	10.1	1166	2 T27075	hypothetical prote
16	118.5	10.1	1208	2 AE1947	chromosome segrega
17	116	9.9	1164	2 T24806	hypothetical prote
18	115	9.8	289	2 S51193	epimorphin - mouse
19	113.5	9.7	1690	2 T13030	microtubule bindin
20	113	9.6	1976	2 A59252	myosin heavy chain
21	113	9.6	1999	1 S21801	myosin heavy chain
22	113	9.6	3187	2 JCS937	364K Golgi complex
23	112.5	9.6	1957	2 T38077	hypothetical coile
24	112	9.6	3685	1 A27605	dystrophin, muscle
25	111.5	9.5	747	1 A57107	kinesin-related pr
26	111.5	9.5	750	2 T38435	coiled coil protei
27	111.5	9.5	857	2 S33821	median body protei
28	111.5	9.5	1178	2 S30431	MSP-300 protein -
29	110.5	9.4	896	2 S43074	epidermal growth f

30	110.5	9.4	924	2 S06117	myosin heavy chain
31	110	9.4	1959	1 A33977	myosin heavy chain
32	109.5	9.3	1992	2 A47297	myosin heavy chain
33	109.5	9.3	2007	1 B43402	myosin heavy chain
34	108.5	9.3	727	2 AC1814	hypothetical prote
35	108.5	9.3	1972	1 A41604	myosin heavy chain
36	108	9.2	464	2 H90279	microtubule bindin
37	108	9.2	734	2 T27055	hypothetical prote
38	108	9.2	1269	2 F84730	probable myosin he
39	107.5	9.2	946	2 S28061	SCP1 protein - rat
40	107.5	9.2	1008	2 AE2304	hypothetical prote
41	107.5	9.2	1509	1 A27224	myosin heavy chain
42	107.5	9.2	1940	2 A59287	myosin heavy chain
43	107.5	9.2	1963	1 MWKW	myosin heavy chain
44	107.5	9.2	2253	2 T30336	nuclear/mitotic ap
45	107	9.1	564	2 A60115	M protein precursor

ALIGNMENTS

RESULT 1

I49508
ISGF3 p91-related transcription factor - mouse
C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49508; I49009
R;Akita, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994

A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr
A;Reference number: A54444; MUID:94208062; PMID:7512451

A;Accession: I49508

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-770 <RES>

A;Cross-references: UNIPROT:P42227; GB:L29278; NID:G476715; PIDN:AAA37254.1; PID:G47671

R;Raz, R.; Durbin, J.E.; Levy, D.E.

J. Biol. Chem. 269, 24391-24395, 1994

A;Title: Acute phase response factor and additional members of the interferon-stimulate

A;Reference number: I49009; MUID:95014185; PMID:7523373

A;Accession: I49009

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-393,'M',395-700,702-770 <RE2>

A;Cross-references: EMBL:U08378; NID:G473889; PIDN:AAA56668.1; PID:G473890

C;Genetics:

A;Gene: APRF

C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 98.6%; Score 1156; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 1.8e-69;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	NHPTAAVTEKQOMLEBQHAQDVVRKRVQDLEQKKVVENLODDDFNYKTLKSGQMDLN 60
DB	130	NHPTAAVTEKQOMLEBQHLQDVVRKRVQDLEQKKVVENLODDDFNYKTLKSGQMDLN 189
QY	61	GNQSVTRQMKQOQLTALDQMRISIVSELAGLLSAMEYVOKTLTDEBLADWKRPEI 120
DB	190	GNQSVTRQMKQOQLTALDQMRISIVSELAGLLSAMEYVOKTLTDEBLADWKRQOI 249
QY	121	ACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELQOKVSKYKGDPIVQHRPMLERI 180
DB	250	ACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELQOKVSKYKGDPIVQHRPMLERI 309
QY	181	VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
DB	310	VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 2

A54444
DNA-binding protein APRF - human

C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A54444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRE, a novel IFN-stimulated gene factor 3 p91-related tra
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
C;Genetics:
A;Gene: GDB:STAT3; APRE
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor

Query Match 98.2%; Score 1151; DB 2; Length 770;
Best Local Similarity 98.3%; Pred. No. 4e-69;
Matches 225; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NHPTAAVTEKQMLEQHAQDVRRKQVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVTEKQMLEQHLQDVRRKQVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

Qy 61 GNNQSVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKTLTDEELADWKRQOI 249

Qy 121 ACIGGPNICLDRLNWTSLAESQLOTRQIKLELQKQSVYKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLNWTSLAESQLOTRQIKLELQKQSVYKGDPIVQHRPMLERI 309

Qy 181 VELFRNLKMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 358

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91- and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 44.9%; Score 526.5; DB 2; Length 739;
Best Local Similarity 46.2%; Pred. No. 1.3e-27;
Matches 104; Conservative 48; Mismatches 60; Indels 13; Gaps 2;

Qy 5 AAVTEKQMLEQHAQDVRRKQVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 64
Db 132 STVMLDKQKELDSKVRNKKVCMKIEHISLEQDQYDFKCTL--QNRHETNVAK 189

Qy 65 SVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEIACIG 124
Db 190 SDQKQEQLLKKVYMLDNRKKEVVKHIIELNVTETQALINDELVEVKKRQOSACIG 249

Qy 125 GPPNICLDRLNWTSLAESQLOTRQIKLELQKQSVYKGDPIVQHRPMLERI 184
Db 310 GPPNICLDRLNWTSLAESQLOTRQIKLELQKQSVYKGDPIVQHRPMLERI 358

Db 250 GPPNACLDLQ-----QVRQQLKLELEQKYTYEHDPIITKNQKQVLWDRTFSLF 298

Qy 185 RNLKMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229
Db 299 QQLIQSFFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKQEL 343

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins
Mol. Cell Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:g509502; PID:AAA19692.1; PID:g50950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 43.6%; Score 511; DB 2; Length 748;
Best Local Similarity 45.5%; Pred. No. 1.4e-26;
Matches 102; Conservative 48; Mismatches 66; Indels 8; Gaps 2;

Qy 8 VTEKQMLEQHAQDVRRKQVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 65
Db 136 VSEQRNVEHKVSAIKNSVQMTEDTKYLEDLQDFDYRYKTIQTMDQGD-----KNSI 189

Qy 66 VTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEIACIG 125
Db 190 LVNQEVLTQLQMLNSLDFKREKLSKMTQIVNETDLLMNSMLEELQDWKKRQOIACIG 249

Qy 126 PPNICLDRLNWTSLAESQLOTRQIKLELQKQSVYKGDPIVQHRPMLERI 185
Db 250 PLHNGLDQQLQNCFTLLAESLFLQRLQLEKLOEQSTKMTVEGDPFPAQRAHLERATFLIY 309

Qy 186 NLKMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229
Db 310 NLFKNSFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 353

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-851 <FU1>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
submitted to the EMBL Data Library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:g1293919; PID:AAA98760.1; PID:g1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in

A:Reference number: S53873; MUID:95192056; PMID:7885841

A:Accession: S53873

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-196;392-591;684-730 <YAW>

A:Cross-references: EMBL:U18671

C:Genetics:

A:Gene: stat2

A:Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 40

C:Superfamily: human signal transducer and transcription activator STAT5A

C:Keywords: signal transduction; transcription regulation

Query Match 27.4%; Score 321; DB 2; Length 851;

Best Local Similarity 33.5%; Pred. No. 7e-14;

Matches 74; Conservative 51; Mismatches 90; Indels 6; Gaps 4;

QY 8 VTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVT 67

DB 138 VSSQHEISRIIDLAMWEKLVKSISQLKDDQDVFCEFRYK-IOAKGKTPSLDPH--QTK 194

QY 68 RQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWRKRPEIACIGGPP 127

DB 195 EQKI--LQETNELDKRRKEVDLASKALLGRLTTLIELLL-PKLEWKAQQKACIRAPI 251

QY 128 NCLDRLENWITSLASSQOTROQIKKLELOQKSYKGDPIVOHRPMLERIVELFRNL 187

DB 252 DHGLEQLEWTFAGAKLLFHLRLKELKSLGSLVSYQDDPLTKGVDLRLNAQVTELLQRL 311

QY 188 MKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLIAVKPE 228

DB 312 LHRFAVVEVQPCMPQTPHRLPILDKTSGKFTVTRLVRLQ 352

RESULT 6

I49274

mammary gland factor - mouse

N:Alternate names: STAT5 protein homolog p80

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49274; S54727

R:Liou X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in

A:Reference number: I49273; MUID:96004632; PMID:7568026

A:Accession: I49274

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-786 <RES>

A:Cross-references: UNIPROT:P42232; UNIPROT:Q9JUM1; EMBL:U21110; NID:g747973; PIDN:AA052

R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A:Reference number: S54772; MUID:95237198; PMID:7720707

A:Accession: S54773

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-432, 'E', 434-786 <MUI>

A:Cross-references: EMBL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636

R:Azam, M.; Brdjlument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,

EMBO J. 14, 1402-1411, 1995

A:Title: Interleukin-3 signals through multiple isoforms of Stat5.

A:Reference number: S54725; MUID:95246733; PMID:7537213

A:Accession: S54727

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-432, 'E', 434-786 <AZA>

C:Genetics:

A:Gene: Stat5b

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.9%; Score 268.5; DB 2; Length 786;

Best Local Similarity 30.6%; Pred. No. 2e-10;

Matches 71; Conservative 42; Mismatches 98; Indels 21; Gaps 5;

QY 5 AAVVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFY-KTLKSGQMDLNGNN 63

DB 134 ADAMSQKHLQINQTFEELRLITQDTENELKLCQTOEYFIIOQESLRIOAQFPAQLGQLN 193

QY 64 -----QSVTRQKMQQLEQML-----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELA 112

DB 194 PORMSRRETALQKQVSLQVETLWQREAOQLQQRVLAEKHQKTLQLLRKQQTILDDLELI 253

QY 113 DWKRPEIACIGGPNICLDRLNENWITSLAESQLQTRQIKKLEELQKSYKGDPIVOHQ 172

DB 254 QMKRRQQLAGNGGPPGSLDLVLSWCEKLAELIWNQRRQIRRAEHLCCQLPIPG-PVEEM 312

QY 173 RPLMEERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLV 224

DB 313 LAENVATITDIISALVTSTFIIIEKQP-----PQVLKATQTKFAATVRLV 356

RESULT 7

S54772

mammary gland factor - mouse

N:Alternate names: stat5 protein

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S54772; I49273

R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A:Reference number: S54772; MUID:95237198; PMID:7720707

A:Accession: S54772

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-793 <MUI>

A:Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA8

R:Liou X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved

A:Reference number: I49273; MUID:96004632; PMID:7568026

A:Accession: I49273

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-793 <RES>

A:Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972

C:Genetics:

A:Gene: Stat5a

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.9%; Score 268.5; DB 2; Length 793;

Best Local Similarity 30.6%; Pred. No. 2e-10;

Matches 70; Conservative 42; Mismatches 96; Indels 21; Gaps 5;

QY 8 VTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFY-KTLKSGQMDLNGNN--- 63

DB 137 MSQKHLQINQTFEELRLITQDTENELKLCQTOEYFIIOQESLRIOAQFPAQLGQLN 196

QY 64 -----QSVTRQKMQQLEQML-----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWK 115

DB 197 RMSRETALQKQVSLQVETLWQREAOQLQQRVLAEKHQKTLQLLRKQQTILDDLELI 256

QY 116 RPETACIGGPNICLDRLNENWITSLAESQLQTRQIKKLEELQKSYKGDPIVOHRPM 175

DB 257 RRQQLAGNGGPPGSLDLVLSWCEKLAELIWNQRRQIRRAEHLCCQLPIPG-PVEEMLA 315

QY 176 LEERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLV 224

DB 316 VNATITDIISALVTSTFIIIEKQP-----PQVLKATQTKFAATVRLV 356

RESULT 8

G02317

transcription activator stat5a - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G02317
R;Lin, J.
Submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBDJB
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g1151169
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.4%; Score 262.5; DB 2; Length 794;
Best Local Similarity 30.1%; Pred. No. 5.1e-10;
Matches 69; Conservative 43; Mismatches 96; Indels 21; Gaps 5;

QY 8 VTEKQMLEHAQDVRRKVDLEQKMKVVENLQDDDFPNY-KTLKSGDMDL----- 59
DB 137 MSQKHLQINQTFEELRVLTQDTELKLLQOTQBYFIIQOESLRIQQAQFAQLNPQE 196
QY 60 NGNNQSVTRQWQMLEQML-----TALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWK 115
DB 197 RLSRETALQKQVSLQVLEAWLQREAGTLOQYRVLEAEKHQKTLQLLRKQOTIILDELLQWK 256
QY 116 RRPFIACGGPNTCLDRLENWITSLSAQLOTRQOIKLEELQKQVSYKGDPIVQHRPM 175
DB 257 RRQLAGNGGPPGSLDVLQSWCEKLAETIWNQRRQIRRAEHLCCQLPIPG-PVEEMLAE 315
QY 176 LEERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLV 224
DB 316 VNATITDIISALVTSFIIEKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 9
S55527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regul
A;Reference number: S55527; MUID:9518889; PMID:7882987
A;Accession: S55527
A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g6023
A;Note: this is a revision to the sequence from reference S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716, 'RHLHGSLPSR', 729, 'P', 731, 'ASL' <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.2%; Score 237; DB 2; Length 794;
Best Local Similarity 29.3%; Pred. No. 2.5e-08;
Matches 67; Conservative 42; Mismatches 98; Indels 22; Gaps 6;

QY 8 VTEKQMLEHAQDVRRKVDLEQKMKVVENLQDDDFPNY-KTLKSGDMDLNGNN--- 63
DB 138 MSQKHLQINQTFEELRVLTQDTELKLLQOTQBYFIIQOESLRIQQAQFAQLNPQE 197
QY 64 ----QSVTRQWQMLEQML-----TALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWK 115
DB 198 RLSRETALQKQVSLQVLEAWLQREAGTLOQYRVLEAEKHQKTLQLLRKQOTIILDELLQWK 257
QY 116 RRPFIACGGPNTCLDRLENWITSLSAQLOTRQOIKLEELQKQVSYKGDPIVQHRPM 175
DB 258 RRHWRGMEAPPR-SLDVLQSWCEKLAETIWNQRRQIRRAEHLCCQLPIPG-PVEEMLAE 315

QY 176 LEERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVV 224
DB 316 VNATITDIISALVTSFIIEKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 10
A54740
interleukin-4-induced transcription factor stat - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
R;Hou, J.; Schindler, U.; Henszel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-848 <HOU>
A;Cross-references: UNIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription regulation

Query Match 10.6%; Score 124.5; DB 2; Length 848;
Best Local Similarity 29.7%; Pred. No. 0.82;
Matches 41; Conservative 22; Mismatches 52; Indels 23; Gaps 4;

QY 88 IVSELAGLSAMEYVQKTLTDEELADWKRPETACTGGPNICLDRLNWLITSLASQLQ 147
DB 182 LLOFTTGELEA---AKALVLKRIQIWKRRQQQLAGNGAP-----FEESLAPLQER 227
QY 148 TRQIKKLEELQKQSVYKGDPI-VQHRPMLLEERIVELFRNLKMSAFVVERQPCMPHDPDR 206
DB 228 CESLVDIYSQLQOEVGAAAGELEPKTRASLTGRLDEVLTSLVTSCLFVEKQP----- 279
QY 207 PLVIKTGVQFTTKVRLVV 224
DB 280 PQVLKTQTKFQAGVRELL 297

RESULT 11
A70387
conserved hypothetical protein aq_1006 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70387
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70387
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-978 <AQF>
A;Cross-references: UNIPROT:O67124; GB:AE000718; NID:g2983504; PIDN:AAC07092.1; PID:g29
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1006
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 10.3%; Score 121; DB 2; Length 978;
Best Local Similarity 23.3%; Pred. No. 1.7;
Matches 49; Conservative 38; Mismatches 81; Indels 42; Gaps 6;

QY 10 EKQMLEHAQDVRRKVDLEQKMKVVENLQDDDFPNYKTLKSGDMDLNGNNQSVTRQ 69
DB 234 EEDSLERELSQQVTKLELENKEVEKLEKLEFSRKVAP-----YVPIAK 281
QY 70 KMQQLQFMTALDQMRRSIVSELAGLSAMEYVQKTLT-----DEELAD- 113
DB 282 RIBEIDKLTTELKVRKNKLTKEALVLKDELSPAQELNRIEAKFKPEKEKEKELEHR 341

Search completed: May 25, 2005, 17:45:29
Job time : 22.6038 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 95.284 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-30

Perfect score: 1172

Sequence: 1 NHPTRAAVTEKQOMLEQHAQ.....IKTGVQFTTKVLLVKFPPEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	DB ID	Description
1	1156	98.6	770	1	STA3_HUMAN	P40763 homo sapien
2	1156	98.6	770	1	STA3_MOUSE	P42227 mus musculus
3	1153	98.4	770	1	STA3_RAT	P52631 rattus norv
4	1149	98.0	770	1	STA3_BOVIN	P61635 bos taurus
5	1131	96.5	771	2	O6DV79	O6dv79 gallus gall
6	1098	93.7	769	2	Q9PVX8	Q9pvx8 xenopus lae
7	1095	93.4	766	2	Q7ZXK3	Q7zxx3 xenopus lae
8	1010	86.2	414	2	Q7ZTS5	Q7zt85 brachydanio
9	1010	86.2	765	2	O6DVF3	O6dvf3 oryzias lat
10	1010	86.2	785	2	O6GUE7	O6gue7 oryzias lat
11	1010	86.2	786	2	O6NV46	O6nv46 brachydanio
12	1010	86.2	806	2	O93599	O93599 brachydanio
13	986	84.1	764	2	Q90Y16	Q90y16 tetraodon f
14	976	83.3	767	2	O13133	O13133 oncorhynch
15	656	56.0	163	2	O9N145	O9n145 macaca mula
16	578	49.3	751	2	O8JGN0	O8jgn0 xenopus lae
17	576	49.1	712	2	Q6PQ07	Q6pq07 rattus norv
18	576	49.1	749	2	Q9QXK0	Q9qxx0 rattus norv
19	574	49.0	749	2	O8C497	O8c497 mus musculus
20	573	48.9	712	2	O99K94	O99k94 mus musculus
21	573	48.9	749	2	O8C3V4	O8c3v4 mus musculus
22	573	48.9	749	2	O9D323	O9d323 mus musculus
23	573	48.9	755	2	O8C8M3	O8c8m3 mus musculus
24	572	48.8	750	1	STA1_HUMAN	P42224 homo sapien
25	572	48.8	750	2	O68D00	O68d00 homo sapien
26	572	48.8	757	2	Q764M5	Q764m5 sus scrofa
27	565	48.2	749	1	STA1_MOUSE	P42225 mus musculus
28	541.5	46.2	754	2	O13131	O13131 oncorhynch
29	535	45.6	749	2	O93598	O93598 brachydanio
30	535	45.6	749	2	Q6P943	Q6p943 brachydanio
31	534	45.6	528	2	O8JFU8	O8jfu8 brachydanio

32	532.5	45.4	108	2	Q704W6	Q704w6 bos taurus
33	530.5	45.3	718	2	Q801Y2	Q801y2 carassius a
34	523	44.6	748	1	STA4_HUMAN	Q14765 homo sapien
35	520.5	44.4	758	2	Q90Y17	Q90y17 tetraodon f
36	518.5	44.4	754	2	O13132	O13132 oncorhynch
37	516	44.0	657	2	O8AW24	O8aw24 brachydanio
38	507.5	43.3	749	1	STA4_MOUSE	P42228 mus musculus
39	507	43.3	651	2	Q7Z253	Q7z253 brachydanio
40	507	43.3	667	2	O8AW20	O8aw20 brachydanio
41	506.5	43.2	652	2	Q7Z277	Q7z277 brachydanio
42	506	43.2	553	2	O8JFU7	O8jfu7 brachydanio
43	506	43.2	748	2	O6GHB2	O6ghb2 rattus norv
44	504	43.0	1153	2	Q8JFS5	Q8jfs5 brachydanio
45	494	42.2	737	2	Q90Y15	Q90y15 tetraodon f

ALIGNMENTS

RESULT 1
STA3_HUMAN
ID STA3_HUMAN STANDARD; PRT; 770 AA.
AC P40763; O14916; Q9BW54;
DT 01-FEB-1995 (Rel. 31, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=STAT3; Synonyms=APRF;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RA Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.,
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RL Cell 77:163-71(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.,
RT "Highly conserved amino-acid sequence between murine STAT3 and a
RL Gene 213:119-124(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "Seattlenseq. NHLBI HL6682 program for genomic applications, UW-
RL FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RN [4]
RP Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
RC TISSUE=Kidney, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 564-704 FROM N.A.
 RP TISSUE=Liver;
 RC Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN PHOSPHORYLATION ON SERINE.
 RP MEDLINE=95215843; PubMed=7701321;
 RA Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
 RT "Requirement of serine phosphorylation for formation of STAT-promoter
 RT complexes";
 RL Science 267:1990-1994(1995).
 RN [7]
 RN INTERACTION WITH NCOAL.
 RP PubMed=1173079; DOI=10.1074/jbc.M11486200;
 RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
 RL "Functional interaction of STAT3 transcription factor with the
 RT coactivator NcoA/SRC1a";
 RA J. Biol. Chem. 277:8004-8011(2002).
 CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes.
 CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P40763-1; Sequence=VSP_010474;
 CC Name=Del-701;
 CC IsoId=P40763-2; Sequence=VSP_010474;
 CC TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
 CC muscle, kidney and pancreas.
 CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, INF-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity.
 CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; L29277; AAA58374.1; -
 CC EMBL; AJ012463; CAAL10032.1; -
 CC EMBL; AY572796; AAS66986.1; -
 CC EMBL; BC000627; AAH00627.1; -
 CC EMBL; BC014482; AAH14482.1; -
 CC EMBL; AF029311; AAB84254.1; -
 CC PIR; A54444; A54444.
 CC HSPSP; P42227; 1BC1.
 CC Genew; HGNC:11364; STAT3.
 CC TRANSFAC; T01493; -
 CC H-InVDB; HIX0013840; -
 CC MIM; 102582; -
 CC GO; GO:0005737; C:cytoplasm; TAS.
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. .; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
 DR GO; GO:0000122; P:negative regulation of transcription from P. .; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR PROSITE; PS00001; SH2; 1.
 KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
 KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
 FT DOMAIN 580 670
 FT MOD_RES 705 705
 FT MOD_RES 727 727
 FT VARSPLIC 701 701
 FT VARIANT 32 32
 FT VARIANT 143 143
 FT VARIANT 143 143
 FT CONFLICT 288 288
 FT CONFLICT 460 460
 FT CONFLICT 548 548
 FT CONFLICT 561 561
 FT CONFLICT 667 667
 FT CONFLICT 730 730
 FT SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
 SQ
 Query Match 98.6%; Score 1156; DB 1; Length 770;
 Best Local Similarity 98.7%; Pred. No. 3.1e-05;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTETKQMLEQHAQDVVKRVQDLQEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVVTETKQMLEQHLQDVVKRVQDLQEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQMQQLEQMLTALDQRRSIVSELQGLLSAMEYVQKTLTDESLADKKRPEI 120
 DB 190 GNNQSVTRQMQQLEQMLTALDQRRSIVSELQGLLSAMEYVQKTLTDESLADKKRQOI 249
 QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQIIKKLELOQKVKYKGDPIVQHRPMLERI 180
 DB 250 ACIGGPPNICLDRLNWTSLAESQLQTRQIIKKLELOQKVKYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 358
 RESULT 2
 STA3 MOUSE
 ID STA3 MOUSE STANDARD; PRT; 770 AA.
 AC P42227;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 GN Name=Stat3; Synonyms=Aprf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
 RP AND 632-640.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;

RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RL Cell 77:63-71(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Thymus;
RX MEDLINE=941188718; PubMed=8140422;
RA Zhong Z., Wen Z., Darnell J.E. Jr.;
RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
RT response to epidermal growth factor and interleukin-6.";
RL Science 264:95-98(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Brain;
RX MEDLINE=95014185; PubMed=7523373;
RA Raz R., Durbin J.E., Levy D.E.;
RT "Acute phase response factor and additional members of the interferon-
RT stimulated gene factor 3 family integrate diverse signals from
RT cytokines, interferons, and growth factors.";
RL J. Biol. Chem. 269:24391-24395(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
RX MEDLINE=96016116; PubMed=7568080;
RA Schaefer T.S., Sanders L.K., Nathans D.;
RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
RT form of Stat3.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=129/SvJ;
RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
RA Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zon L., Oka T.,
RA Dewar K., Hennighausen L.;
RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
RT zebrafish to mouse.";
RL Genomics 71:150-155(2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=C57BL/60, and NOD/LtJ;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shennan C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Dapkinenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.

RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
RA Wen Z., Zhong Z., Darnell J.E. Jr.;
RT "Maximal activation of transcription by Stat1 and Stat3 requires both
RT tyrosine and serine phosphorylation.";
RL Cell 82:241-250(1995).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
RA Becker S., Groner B., Mueller C.W.;
RT "Three-dimensional structure of the Stat3beta homodimer bound to
RT DNA.";
RL Nature 394:145-151(1998).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes. STAT3B interacts with the N-terminal
CC part of JUN to activate such promoters in a cooperative way.
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (by similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Stat3A;
CC IsoId=P42227-1; Sequence=Displayed;
CC Name=Stat3B;
CC IsoId=P42227-2; Sequence=VSP_006287;
CC Name=Del-701;
CC IsoId=P42227-3; Sequence=VSP_010475;
CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
CC kidney. STAT3B is also detected in the liver, although in a much
CC less abundant manner.
CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC
CC "This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L29278; AAA37254.1; --
CC EMBL; U06922; AAA19452.1; --
CC EMBL; U08378; AAA56668.1; --
CC EMBL; U30709; AAC52612.1; --
CC EMBL; AF246978; AAL59017.1; --
CC EMBL; AY299489; AAQ75418.1; --
CC EMBL; AY299490; AAQ75419.1; --
CC EMBL; BC003806; AAH03806.1; --
CC PIR; I49508; I49508.
CC PDB; 1BG1; X-ray; A=1-722.
CC TRANSFAC; T01574; --
CC MGD; MGI:103038; Stat3.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0003677; F:DNA binding; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0016563; F:transcriptional activator activity; IDA.
CC GO; GO:0007259; P:JAK-STAT cascade; IDA.
CC GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
CC InterPro; IPR008967; P53 like_DNA_bnd.
CC InterPro; IPR000980; SH2
CC InterPro; IPR001217; STAT.
CC Pfam; PF00017; SH2; 1.
CC Pfam; PF01017; STAT_alpha; 1.
CC Pfam; PF02864; STAT_bind; 1.

```

DR Pfam; PF02865; STAT int; 1.
DR PROSITE; PS50001; SH2; 1.
KW 3D-structure; Activator; Acute phase; Alternative splicing;
KW Direct protein sequencing; DNA-binding; Nuclear protein;
KW Phosphorylation; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine.
FT VARSPPLIC 716 770 TTCSNTIDLPMSPTSLDLSLMQFGNGEGAPSPAGGQFESLT
FT FMDLTSECATSPM -> FIDAVWK (in isoform
FT Stat3B).
FT FTID=VSP_006287.
FT Missing (in isoform Del-701).
FT FTID=VSP_010475.
FT S-A: Decreased transcriptional
FT activation.
FT 16 16
FT CONFLICT 25 25 E -> K (in Ref. 2).
FT CONFLICT 394 394 S -> T (in Ref. 2 and 4).
FT HELIX 139 180 M -> I (in Ref. 1).
FT TURN 181 182
FT TURN 197 198
FT HELIX 199 237
FT TURN 238 238
FT HELIX 239 251
FT TURN 252 253
FT HELIX 261 290
FT TURN 294 295
FT TURN 297 301
FT HELIX 302 320
FT TURN 321 328
FT STRAND 330 331
FT TURN 333 334
FT TURN 336 337
FT STRAND 338 340
FT TURN 341 342
FT STRAND 345 351

Query Match 98.6%; Score 1156; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.1e-65;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMODLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMODLN 189

QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRQOI 249

QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVSYGKDPPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVSYGKDPPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 3
STA3 RAT STANDARD; PRT; 770 AA.
ID _STA3 RAT
AC PS2631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=stat3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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STA3_BOVIN
ID STA3_BOVIN STANDARD; PRT; 770 AA.
AC P61635;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=STAT3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
ON NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RT "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
during ruminant evolution."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
acute-phase protein genes (By similarity).
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
member (at least STAT1). Interacts with NCOAL (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
in response to phosphorylation (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ620655; CAF06182.1; -.
DR PROSITE; P55001; SH2; 1.
KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73B83274 CRC64;
Query Match 98.0%; Score 1149; DB 1; Length 770;
Best Local Similarity 98.3%; Pred. No. 8.6e-65;
Matches 225; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQMLEQHAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQMLEQHAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPR 120
DB 190 GNNQSVTRQKMQQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQ 249
QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLELOQKVSYGKDPVQHRPMLER 180
DB 250 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLELOQKVSYGKDPVQHRPMLER 309
QY 181 VELFRNLKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 358
RESULT 5
Q6DV79
ID Q6DV79 PRELIMINARY; PRT; 771 AA.
AC Q6DV79;

DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Signal transducer and activator of transcription 3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
ON NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641397; AAT64887.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS5001; SH2; 1.
SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;
Query Match 96.5%; Score 1131; DB 2; Length 771;
Best Local Similarity 96.9%; Pred. No. 1.2e-63;
Matches 221; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2 HPTAAVTEKQMLEQHAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 61
DB 131 HPTAAVTEKQMLEQHAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 190
QY 62 NNQSVTRQKMQQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIA 121
DB 191 NNQSVTRQKMQQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQ 250
QY 122 CIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLELOQKVSYGKDPVQHRPMLER 181
DB 251 CIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLELOQKVSYGKDPVQHRPMLER 310
QY 182 ELFRNLKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 229
DB 311 ELFRNLKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 358
RESULT 6
Q9PVX8
ID Q9PVX8 PRELIMINARY; PRT; 769 AA.
AC Q9PVX8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Stat 3.
GN Name=stat 3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
ON NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
RA Asashima M., Yokota T.;
RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
embryos independent of BMP-4."
RL Dev. Biol. 216:481-490(1999).
DR EMBL; AB017701; BAA86061.1; -.

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udwin T.B., Tothyluki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-AB; TISSUE-Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045276; AAH45276.1; -;
DR HSSP; P42227; 1BG1.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 414 AA; 748253 MW; 0FFD1B509B7526BD CRC64;

Query Match 86.2%; Score 1010; DB 2; Length 414;
Best Local Similarity 84.3%; Pred. No. 2.9e-56;
Matches 194; Conservative 21; Mismatches 13; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLQHAQDVRRKQVQDLQKQKMKVVENLQDDFDNFYKTLKSGQDM-QDLN 60
DB 130 HPTGTVVTEKQQLLEHNLDIRKRVQDMQKMKLENLQDDFDNFYKTLKSGQDLN 189
QY 61 GNNQ-SVTRQKMQQLQMLTALDQMRSSIVSELGALLSMEYVQKTLTDEELADWKRRPE 119
DB 190 GNSQAATRKQMSQLQMLQMLSDQLRRQIVTEMAGLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQSVYKGDPIVQHRPMLER 179
DB 250 IACIGPPNICLDRLTWTSLAESQLQIRQIKLEELQKQSVYKGDPIIHRPALEEK 309
QY 180 IVELFRLMKSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 229
DB 310 IVDLFRLMKSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 359

RESULT 9
Q6DVF3
ID Q6DVF3 PRELIMINARY; PRT; 765 AA.
AC Q6DVF3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Signal transducer and activation of transcription factor 3.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RN SEQUENCE FROM N.A.
RL Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY639947; AAT64912.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;
Query Match 86.2%; Score 1010; DB 2; Length 765;
Best Local Similarity 84.3%; Pred. No. 5.6e-56;
Matches 194; Conservative 20; Mismatches 14; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLQHAQDVRRKQVQDLQKQKMKVVENLQDDFDNFYKTLKSGQDM-QDLN 60
DB 130 HPTGTVVTEKQQLLEHNLDIRKRVQDMQKMKLENLQDDFDNFYKTLKSGQDLN 189
QY 61 GNNQ-SVTRQKMQQLQMLTALDQMRSSIVSELGALLSMEYVQKTLTDEELADWKRRPE 119
DB 190 GNSQAATRKQMSQLQMLQMLSDQLRRQIVTEMAGLLTAMDYVQKNTLDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQSVYKGDPIVQHRPMLER 179
DB 250 IACIGPPNICLDRLTWTSLAESQLQIRQIKLEELQKQSVYKGDPIIHRPALEEK 309
QY 180 IVELFRLMKSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 229
DB 310 IVDLFRLMKSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 359

RESULT 10

Q6GUE7

ID Q6GUE7

AC Q6GUE7

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Signal transducer and activator of transcription 3 isoform 1.

OS Oryzias latipes (Medaka fish) (Japanese ricefish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

OX NCBI_TaxID=8090;

RN [1]
RN SEQUENCE FROM N.A.

RL Liu R., Hong Y.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY641434; AAT46364.1; -;

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR InterPro; IPR008967; P53 like_DNA_bnd.

DR InterPro; IPR000980; SH2

DR InterPro; IPR001217; STAT.

DR Pfam; PF01017; SH2; 1.

DR Pfam; PF01017; STAT_alpha; 1.

DR Pfam; PF02864; STAT bind; 1.
DR Pfam; PF02865; STAT int; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;

Query Match 86.2%; Score 1010; DB 2; Length 785;
Best Local Similarity 84.3%; Pred. No. 5.7e-56;
Matches 194; Conservative 20; Mismatches 14; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEQHAQDVKRVQDLQKQKVVENLQDDFDNFYKTLKSQGM-ODLN 60
DB 130 HPTGTVVTEKQMLEHNLQDQIRKRVQDMQKMKLENLQDDFDNFYKTLKSQGLNQLN 189
QY 61 GNNQ-SVTRQKQMLEQMLTALDQMRISVSELQGLLSAMEYVOKLTDEELADWKRRPE 119
DB 190 GNSQAAATQKMAQLEQMLTALDQMRISVSELQGLLSAMEYVOKLTDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKQVYKGDPIVQHRPMLER 179
DB 250 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKQVYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 359

RESULT 11

Q6NV46 PRELIMINARY; PRT; 786 AA.
AC Q6NV46;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Mairra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC068320.1; -.
RL ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF001017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT bind; 1.
DR Pfam; PF02865; STAT int; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;

Query Match 86.2%; Score 1010; DB 2; Length 786;
Best Local Similarity 84.3%; Pred. No. 5.7e-56;
Matches 194; Conservative 21; Mismatches 13; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEQHAQDVKRVQDLQKQKVVENLQDDFDNFYKTLKSQGM-ODLN 60
DB 130 HPTGTVVTEKQMLEHNLQDQIRKRVQDMQKMKLENLQDDFDNFYKTLKSAGELSQDLN 189
QY 61 GNNQ-SVTRQKQMLEQMLTALDQMRISVSELQGLLSAMEYVOKLTDEELADWKRRPE 119
DB 190 GNSQAAATQKMSQLEQMLTALDQMRISVSELQGLLSAMEYVOKLTDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKQVYKGDPIVQHRPMLER 179
DB 250 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKQVYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 359

RESULT 12
O93599 PRELIMINARY; PRT; 806 AA.
AC O93599;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oates A.C.;
RL Thesis (1998), University of Melbourne, Australia.
RL EMBL; AJ005693; CAA06677.1; -.
DR HSSP; P42227; IBGI.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF001017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT bind; 1.
DR Pfam; PF02865; STAT int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match 86.2%; Score 1010; DB 2; Length 806;
Best Local Similarity 84.3%; Pred. No. 5.9e-56;


```
Matches 194; Conservative 21; Mismatches 13; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHAQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDL 60
Db 130 HPTGTVTEKQMLEHNLQDQIRKRVQDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDLN 189
QY 61 GNNQ-SVTRQKMQLEQMLTALDOMRSIVSELAGLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLTALDOMRSIVTEMAGLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEEQKVSQYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEEQKVSQYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPDRPLVIKGTGVQFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPDRPLVIKGTGVQFTTKVRLLVKFPPEL 359

RESULT 13
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF001017; SH2; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661PFE18B8FD8BE CRC64;

Query Match 84.1%; Score 986; DB 2; Length 764;
Best Local Similarity 83.0%; Pred. No. 1.8e-54;
Matches 191; Conservative 21; Mismatches 16; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHAQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDL 60
Db 130 NPSTGVTEKQMLENLQDQIRKRVQDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDLN 189
QY 61 GNNQ-SVTRQKMQLEQMLTALDOMRSIVSELAGLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLTALDOMRSIVTEMAGLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEEQKVSQYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEEQKVSQYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPDRPLVIKGTGVQFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPDRPLVIKGTGVQFTTKVRLLVKFPPEL 359

Query Match 84.1%; Score 986; DB 2; Length 764;
Best Local Similarity 83.0%; Pred. No. 1.8e-54;
Matches 191; Conservative 21; Mismatches 16; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHAQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDL 60
Db 130 NPSTGVTEKQMLENLQDQIRKRVQDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDLN 189
QY 61 GNNQ-SVTRQKMQLEQMLTALDOMRSIVSELAGLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLTALDOMRSIVTEMAGLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEEQKVSQYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEEQKVSQYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPDRPLVIKGTGVQFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPDRPLVIKGTGVQFTTKVRLLVKFPPEL 359
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RESULT 14
O13133 PRELIMINARY; PRT; 767 AA.
AC O13133;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
GN NamesrbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match 83.3%; Score 976; DB 2; Length 767;
Best Local Similarity 81.0%; Pred. No. 8e-54;
Matches 187; Conservative 25; Mismatches 17; Indels 2; Gaps 2;
QY 1 NHPTAAVTEKQMLEQHAQDVRRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDL 59
Db 129 SHPSGTVTTEKQMLEHNLQDQIRKRVQDMQKMKMLNQLQDDFDNFYKTLKSAGLSQDM 188
QY 60 GNNQ-SVTRQKMQLEQMLTALDOMRSIVSELAGLSAMEYVQKTLTDEELADWKRRP 118
Db 189 GNSQAARQKMAQLEQMLTALDOMRSIVTEMAGLSAMDVFQKNTLDEELADWKRRQ 248
QY 119 ETACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEEQKVSQYKGDPIVQHRPMLER 178
Db 249 QIACIGGPPKICLDRLETWITSLSAQLOTRQOIKKLEEQKVSQYKGDPIVQHRPMLER 308
QY 179 RIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKGTGVQFTTKVRLLVKFPPEL 229
Db 309 KIVDLFRNLKMSAFVVERQPCMPHDPDRPLVIKGTGVQFTTKVRLLVKFPPEL 359

RESULT 15
Q9N145 PRELIMINARY; PRT; 163 AA.
AC Q9N145;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Name-STAT3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
```

DR EMBL; AF227560; AAF73401.1; --
DR HSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
FT NON_TER 1
FT TER 163
SQ SEQUENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;

Query Match 56.0%; Score 656; DB 2; Length 163;
Best Local Similarity 98.4%; Pred. No. 2.9e-34;
Matches 126; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 102 VQKTLTDEELADWKRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOK 161
Db 1 VQKTLTDEELADWKRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOK 60

Qy 162 VSYKGDPIVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMPDRPLVIKTVQFTTKVR 221
Db 61 VSYKGDPIVQHRPMLERIIVELFRNLKMSAFVVERQPCMPMPDRPLVIKTVQFTTKVR 120

Qy 222 LLVKFPPEL 229
Db 121 LLVKFPPEL 128

Search completed: May 25, 2005, 17:43:44
Job time : 96.284 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 121.891 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-31

Perfect score: 1172

Sequence: 1 NIPATAVTEKQQLMLQHQHLO.....IKTGVOFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1172	100.0	229	4 AAY72863	Aay72863 Mouse Sta
2	1168	99.7	229	4 AAY72850	Aay72850 Mouse Sta
3	1168	99.7	252	4 AAY72846	Aay72846 Mouse Sta
4	1168	99.7	271	4 AAY72841	Aay72841 Mouse Sta
5	1168	99.7	770	2 AAY72082	Aay72082 Mouse Sta
6	1168	99.7	770	2 AAW03176	Aaw03176 Mouse Sta
7	1163	99.2	229	4 AAY72862	Aay72862 Mouse Sta
8	1157.5	98.8	228	4 AAY72861	Aay72861 Mouse Sta
9	1157	98.7	720	5 AAE22055	Aae22055 Human Sta
10	1157	98.7	769	5 ABE57164	Abbe57164 Mouse isc
11	1157	98.7	769	5 AAE22054	Aae22054 Human Sta
12	1157	98.7	769	5 AAE22056	Aae22056 Human pro
13	1157	98.7	770	2 AAR82995	Aar82995 Mouse liv
14	1157	98.7	770	2 AAY03768	Aay03768 Human STA
15	1157	98.7	770	3 AAB12377	Aab12377 N-termina
16	1157	98.7	770	5 AAE14652	Aae14652 Murine ST
17	1157	98.7	770	5 ABG69497	Abg69497 Human bai
18	1157	98.7	770	6 ABUI0476	Abui0476 Mouse STA
19	1157	98.7	770	8 ADN04365	Adn04365 Antipsori
20	1157	98.7	770	8 ADP54789	Adp54789 Human PRO
21	1157	98.7	793	3 AAB58442	Aab58442 Lung canc
22	1154	98.5	770	7 ADD44738	Add44738 Rat Prote
23	1152	98.3	770	2 AAR82993	Aar82993 Human pia
24	1152	98.3	770	4 AAB19964	Aab19964 Human sig
25	1152	98.3	770	5 AAE15174	Aae15174 Human Sta

26	1152	98.3	770	7	ADD44740	Add44740 Human Pro
27	1150	98.1	229	4	AAY72860	Aay72860 Mouse Sta
28	1090	93.0	213	4	AAY72851	Aay72851 Mouse Sta
29	1090	93.0	236	4	AAY72847	Aay72847 Mouse Sta
30	1044	89.1	223	4	AAY72854	Aay72854 Mouse Sta
31	845	72.1	185	4	AAY72855	Aay72855 Mouse Sta
32	777	66.3	176	4	AAY72848	Aay72848 Mouse Sta
33	653	55.7	128	4	AAY72852	Aay72852 Mouse Sta
34	601	51.3	143	4	AAY72849	Aay72849 Mouse Sta
35	573	48.9	749	5	AAG78526	Aag78526 Rat STAT-
36	571	48.7	129	4	AAY72856	Aay72856 Mouse Sta
37	569	48.5	268	4	AAY72844	Aay72844 Mouse Sta
38	569	48.5	582	2	AAW62996	Aaw62996 Human tru
39	569	48.5	582	6	ABU04748	Abu04748 Human exp
40	569	48.5	582	8	ADH57036	Adh57036 Truncated
41	569	48.5	680	6	ABR59713	Abr59713 Human sig
42	569	48.5	712	2	AAR72079	Aar72079 Human sig
43	569	48.5	712	2	AAW03170	Aaw03170 Human STA
44	569	48.5	712	2	AAW62995	Aaw62995 Human STA
45	569	48.5	712	6	ABU04747	Abu04747 Human exp

ALIGNMENTS

RESULT 1

AAV72863

ID AAY72863 standard; protein; 229 AA.

AC AAY72863;

DT 31-MAY-2001 (first entry)

DE Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).

KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; mutein.

OS Mus musculus.

FH Key Location/Qualifiers

FT Region 1..25

FT /notes= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"

FT Misc-difference 22

FT /note= "wild type Val substituted with Ala corresponds to
151 position of Stat-3 protein"

FT Region 213..229

FT /note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"

PN WO200116605-A2.

PD 08-MAR-2001.

PF 30-AUG-2000; 2000WO-US023822.

PR 31-AUG-1999; 99US-00387418.

PA (UYRQ) UNIV ROCKEFELLER.

PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;

DR WPI; 2001-226705/23.

XX Identifying an agent for use in modulating the interaction between
transcription factor c-Jun and a Stat3 protein.

PS Claim 66; Page 86; 86pp; English.

XX The present sequence is mouse Stat3 mutant (V151A) protein fragment
containing 130-358 amino acids of Stat3 protein. This mutant is obtained

CC by replacing Val 151 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 CC
 XX Sequence 229 AA;

Query Match 100.0%; Score 1172; DB 4; Length 229;
 Best Local Similarity 100.0%; Pred. No. 6.5e-100;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGDMQDLN 60
 DB 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGDMQDLN 60
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 DB 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLEELQKVSFKGDPVQHRPMLLEERI 180
 DB 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLEELQKVSFKGDPVQHRPMLLEERI 180
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229
 DB 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229

RESULT 2
 AAY72850
 ID AAY72850 standard; protein; 229 AA.

XX AAY72850;
 AC
 DT 31-MAY-2001 (first entry)
 DE Mouse Stat3 protein fragment #8 (130-358 amino acids).
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FH Region 1. .25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 213. .229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX WO200116605-A2.

XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 DR WPT; 2001-226705/23.
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.

XX Claim 65; Page 76-77; 86pp; English.
 PS The present sequence is mouse Stat3 protein fragment containing 130-358
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 CC
 XX Sequence 229 AA;

Query Match 99.7%; Score 1168; DB 4; Length 229;
 Best Local Similarity 99.6%; Pred. No. 1.5e-99;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGDMQDLN 60
 DB 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGDMQDLN 60
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 DB 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLEELQKVSFKGDPVQHRPMLLEERI 180
 DB 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLEELQKVSFKGDPVQHRPMLLEERI 180
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229
 DB 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229

RESULT 3
 AAY72846

ID AAY72846 standard; protein; 252 AA.
 XX AAY72846;
 AC
 DT 31-MAY-2001 (first entry)
 DE Mouse Stat3 protein fragment #4 (107-358 amino acids).
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FH Region 24. .48
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 236. .252
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX WO200116605-A2.
 XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;

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XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 65; Page 73; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-358
XX amino acids of Stat3 protein. This Stat3 fragment showed strong binding
XX to c-Jun protein in the cell extract. The invention relates to methods
XX for identifying interacting regions of transcription factors and methods
XX for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 252 AA;
XX
XX Query Match 99.7%; Score 1168; DB 4; Length 252;
XX Best Local Similarity 99.6%; Pred. No. 1.7e-99;
XX Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 NHPTAAVVTKEQMLQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
XX Db 24 NHPTAAVVTKEQMLQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 83
XX
XX 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
XX Db 84 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 143
XX
XX 121 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEELQKYSYKGDPIVQHRPMLLEERI 180
XX Db 144 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEELQKYSYKGDPIVQHRPMLLEERI 203
XX
XX 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEEL 229
XX Db 204 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEEL 252
XX
XX RESULT 4
XX AAY72841
XX ID AAY72841 standard; protein; 271 AA.
XX AC AAY72841;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 protein fragment #2 (107-377 amino acids).
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX cellular transformation; dysproliferative disease; cancer; psoriasis;
XX therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Region 24..48
XX FT /notes="Stat3-c-Jun interaction region 1; corresponds to
XX FT 130-154 position of Stat3 protein"
XX FT 236..252
XX FT /notes="Stat3-c-Jun interaction region 2; corresponds to
XX FT 342-358 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
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PR 31-AUG-1999; 99US-00387418.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wzesszcynska MH, Darnell JE;
XX
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 65; Page 67-68; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-377
XX amino acids of Stat3 protein. This Stat3 fragment showed strong binding
XX to c-Jun protein in the cell extract. The invention relates to methods
XX for identifying interacting regions of transcription factors and methods
XX for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 271 AA;
XX
XX Query Match 99.7%; Score 1168; DB 4; Length 271;
XX Best Local Similarity 99.6%; Pred. No. 1.9e-99;
XX Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 NHPTAAVVTKEQMLQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
XX Db 24 NHPTAAVVTKEQMLQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 83
XX
XX 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
XX Db 84 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 143
XX
XX 121 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEELQKYSYKGDPIVQHRPMLLEERI 180
XX Db 144 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEELQKYSYKGDPIVQHRPMLLEERI 203
XX
XX 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEEL 229
XX Db 204 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEEL 252
XX
XX RESULT 5
XX AAR72082
XX ID AAR72082 standard; protein; 770 AA.
XX AC AAR72082;
XX
XX 25-MAR-2003 (revised)
XX DT 27-SEP-1995 (first entry)
XX
XX Mouse Stat3 (198f6).
XX
XX Signal transducer and activator of transcription; STAT; 198f6; Stat3;
XX receptor recognition factor; transcription factor; cellular debilitation;
XX derangement; dysfunction; interferon-gamma.
XX
XX Mus sp.
XX
XX WO9508629-A1.
XX
XX 30-MAR-1995.
XX
XX 26-SEP-1994; 94WO-US010849.
XX
XX 24-SEP-1993; 93US-00126588.
XX PR 24-SEP-1993; 93US-00126595.
XX
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PR 11-MAR-1994; 94US-00212184.
PR 11-MAR-1994; 94US-00212185.
XX PA (UYRQ) UNIV ROCKEFELLER.
XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
PI WPI; 1995-139598/18.
DR N-PSDB; AAQ89340.
XX Receptor recognition factor implicated in transcriptional stimulation of
PT genes - useful in drug screening assays and/or for treating cellular
PT debilitations, derangements and/or dysfunctions, etc.
XX Claim 1; Page 107-110; 160pp; English.
XX A fragment encoding the human Stat91 protein was used to screen a murine
CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
CC mouse gene as probe, 2 additional members of the 113-91 family of
CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
CC -40) were cloned in plasmids 136f1 and 19sf6 and encoded proteins termed
CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 770 AA;
Query Match 99.7%; Score 1168; DB 2; Length 770;
Best Local Similarity 99.6%; Pred. No. 7.5e-99;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNYKTLKSGDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDPFDNYKTLKSGDMQDLN 189
Qy 61 GNNQSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 120
Db 190 GNNQSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 249
Qy 121 ACIGGPNICLDRLNWNITSLAESQLQTRQIQIKLEELQOKVSYKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLNWNITSLAESQLQTRQIQIKLEELQOKVSYKGDPIVQHRPMLERI 309
Qy 181 VELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL 229
Db 310 VELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL 358
RESULT 6
AAW03176
ID AAW03176 standard; protein; 770 AA.
XX AAW03176;
XX 24-OCT-1996 (first entry)
XX Mouse STAT4.
XX STAT; STAT4; signal transducer and activator of transcription;
KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
KW autoimmune disease; antagonist; therapy.
XX Mus sp.
XX Key Location/Qualifiers
FT Domain 398..508
FT /label= DNA binding domain
FT /note= "Claim 3, page 110"
XX
XX WO9620954-A2.
XX
XX 11-JUL-1996.

XX 28-DEC-1995; 95WO-US017025.
XX PF
XX 06-JAN-1995; 95US-00369796.
XX PA (UYRQ) UNIV ROCKEFELLER.
XX Darnell JE, Wen Z, Horvath CM, Zhong Z;
PI WPI; 1996-333941/33.
DR N-PSDB; AAT31280.
XX New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
PT preventing or treating cellular dysfunction, e.g. oncogenesis,
PT inflammation, parasitic disease or autoimmunity.
XX Disclosure; Page 87-90; 138pp; English.
XX Mouse signal transducer and activator of transcription (STAT) protein
CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
CC ligand-activated receptor kinase complexes followed by nuclear
CC translocation and DNA binding to activate transcription. Recombinant
CC STAT4 can be obt'd. using cDNA clone 19sf6 (AAT31278) obt'd. from
CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
CC AAW03167) capable of both receptor recognition and message delivery via
CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
CC DNA binding domains (see also AAW03165-75) are useful for screening
CC antagonists used to inhibit STAT-mediated signal transduction and
CC activation of transcription
XX
SQ Sequence 770 AA;
Query Match 99.7%; Score 1168; DB 2; Length 770;
Best Local Similarity 99.6%; Pred. No. 7.5e-99;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNYKTLKSGDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDPFDNYKTLKSGDMQDLN 189
Qy 61 GNNQSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 120
Db 190 GNNQSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPEI 249
Qy 121 ACIGGPNICLDRLNWNITSLAESQLQTRQIQIKLEELQOKVSYKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLNWNITSLAESQLQTRQIQIKLEELQOKVSYKGDPIVQHRPMLERI 309
Qy 181 VELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL 229
Db 310 VELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL 358
RESULT 7
AAW72862
ID AAY72862 standard; protein; 229 AA.
XX AAY72862;
XX 31-MAY-2001 (first entry)
XX Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformati; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; mutein.
XX Mus musculus.
XX Key Location/Qualifiers
FT Region 1..25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"

```

FT Misc-difference 19
FT /note= "Wild type Leu substituted with Ala; corresponds
FT to 148 position of Stat-3 protein"
FT Region
FT 213. .229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
XX 31-AUG-1999; 99US-00387418.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 66; Page 85; 86pp; English.
XX
XX The present sequence is mouse Stat3 mutant (L148A) protein fragment
XX containing 130-358 amino acids of Stat3 protein. This mutant is obtained
XX by replacing Leu 148 with Ala in Stat3 protein. The invention relates to
XX methods for identifying interacting regions of transcription factors and
XX methods for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 229 AA;

Query Match 99.2%; Score 1163; DB 4; Length 229;
Best Local Similarity 99.1%; Pred. No. 4.4e-99;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEKQMLSEQLQDARKRVQDLEQKMKVVENLQDDDFDNFKYTKLSQGDMDQLN 60
DB 1 NHPTAAVVTKEKQMLSEQLQDARKRVQDLEQKMKVVENLQDDDFDNFKYTKLSQGDMDQLN 60
QY 61 GNNQSVTRQKMQOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB 61 GNNQSVTRQKMQOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
QY 121 ACIGGPPNICLDRLENWITSLSAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLEREI 180
DB 121 ACIGGPPNICLDRLENWITSLSAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLEREI 180
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGTQFTTKVRLLVKPEPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGTQFTTKVRLLVKPEPEL 229

RESULT 8
ID AAY72861
XX AAY72861 standard; protein; 228 AA.
AC AAY72861;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 mutant (T346A, K348A, R350A) protein fragment.
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX cellular transformation; dysproliferative disease; cancer; psoriasis;
KW

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KW therapy; mutant; mutein.
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Region 1. .25
XX /note= "Stat3-c-Jun interaction region 1; corresponds to
XX 130-154 position of Stat3 protein"
XX Region 213. .229
XX /note= "Stat3-c-Jun interaction region 2; corresponds to
XX 342-358 position of Stat3 protein"
XX Misc-difference 217
XX /note= "Wild type Thr substituted with Ala; corresponds
XX to 346 position of Stat-3 protein"
XX Misc-difference 219
XX /note= "Wild type Lys substituted with Ala; corresponds
XX to 348 position of Stat-3 protein"
XX Misc-difference 221
XX /note= "Wild type Arg substituted with Ala; corresponds
XX to 350 position of Stat-3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023822.
XX
XX 31-AUG-1999; 99US-00387418.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 66; Page 84-85; 86pp; English.
XX
XX The present sequence is mouse Stat3 mutant protein fragment containing
XX 130-358 amino acids of Stat3 protein. This mutant is obtained by
XX replacing Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the
XX Stat3 protein. The invention relates to methods for identifying
XX interacting regions of transcription factors and methods for identifying
XX agents which modulates the interaction between a transcription factor
XX such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for
XX modulating gene transcription e.g., cellular transformation. These
XX identifying agents are used in the treatment of dysproliferative diseases
XX and also for treating cancer and psoriasis. A Stat protein comprises the
XX N-terminal domain, coiled-coil domain, DNA binding domain, linker domain,
XX SH2 domain and transactivation domain
XX
XX Sequence 228 AA;

Query Match 98.8%; Score 1157.5; DB 4; Length 228;
Best Local Similarity 99.6%; Pred. No. 1.4e-98;
Matches 228; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 NHPTAAVVTKEKQMLSEQLQDARKRVQDLEQKMKVVENLQDDDFDNFKYTKLSQGDMDQLN 60
DB 1 NHPTAAVVTKEKQMLSEQLQDARKRVQDLEQKMKVVENLQDDDFDNFKYTKLSQGDMDQLN 59
QY 61 GNNQSVTRQKMQOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB 60 GNNQSVTRQKMQOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 119
QY 121 ACIGGPPNICLDRLENWITSLSAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLEREI 180
DB 120 ACIGGPPNICLDRLENWITSLSAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLEREI 179
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGTQFTTKVRLLVKPEPEL 229

```

Db 180 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 228

RESULT 9
AAE22055
ID AAE22055 standard; protein; 720 AA.

AC AAE22055;

XX 25-JUL-2002 (first entry)

DT Human Stat3beta protein.

DE Human; signal transducer and activator of transcription 3; ischaemia;
KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
KW shock; chronic active hepatitis; adult respiratory distress syndrome;
KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 713..714

FT /note= "Encoded by ACA CCA TTC"

XX WO200220032-A1.

XX 14-MAR-2002.

XX 10-SEP-2001; 2001WO-US028254.

XX 08-SEP-2000; 2000US-0231212P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Yu H, Pardoll D, Jove R, Dalton W;

XX WPI; 2002-362218/39.

XX N-PSDB; AAD35066.

XX Modulating angiogenesis and an immune response in an individual, for

XX treating a hypoxic or ischemic condition, comprises administering a

XX compound that modulates the activity of a signal transducer and activator

XX of transcription 3.

XX Disclosure; Page 87-89; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
XX response. Method involves administering to an individual a compound that
XX modulate the activity of signal transducer and activator of transcription
XX 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
XX hypoxic or ischaemic condition or disorder which is the result of stroke,
XX ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
XX tissue ischaemia in the lower extremities, infarction, trauma, vascular
XX occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
XX chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
XX epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
XX nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
XX with neovascularisation. Suppressing an immune response is useful for
XX ameliorating a symptom of an autoimmune disease such as systemic lupus
XX erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
XX Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
XX mixed connective tissue disease, primary biliary cirrhosis, pernicious
XX anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
XX gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,

CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
CC dense deposit disease. The method is useful in preventing or treating
CC specific proliferative and oncogenic disease which includes sarcomas and
CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
CC hypoproliferative disorders, physical trauma, lesions and wounds. The
CC method is also used in gene therapy. The present sequence is human
CC Stat3beta protein

XX Sequence 720 AA;

SQ Query Match 98.7%; Score 1157; DB 5; Length 720;

Best Local Similarity 98.7%; Pred. No. 7.2e-98;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDARKVODLEQKVKVVENLODDFDFNYKTLKSGQDMQDLN 60

Db 130 NHPTAAVTEKQOMLEQHLQDARKVODLEQKVKVVENLODDFDFNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMOQLEQMLTALQDMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120

Db 190 GNNQSVTRQKMOQLEQMLTALQDMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRQOI 249

QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLPEERI 180

Db 250 ACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLPEERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229

Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 358

RESULT 10

ABB57164

ID ABB57164 standard; protein; 769 AA.

XX AC

XX ABB57164;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related protein sequence SEQ ID NO:398.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX Mus musculus.

XX WO200188188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP004192.

XX 18-MAY-2000; 2000JP-00145977.

XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

XX N-PSDB; ABI99454.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring

XX expression levels of particular genes defined in the specification or by

XX determining the expression profile of a gene group comprising these

XX genes.

XX Claim 2; Page 1084-1087; 2690pp; English.

XX The present invention describes a method for examining ischaemic

CC conditions, comprising measuring the expression levels of particular

CC genes (1) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (1). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI9912, encoding the
 CC protein sequences in ABBS7020 to ABBS7374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI9913 and ABI9914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention

XX Sequence 769 AA;

Query Match 98.7%; Score 1157; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 7.8e-98;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDARKVRVDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDARKVRVDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDELDADWKRPEI 120
 DB 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDELDADWKRPEI 249

QY 121 ACIGGPPNCLDRLENWITS LAESQLQTRQIKLEELQKQVSKYKGDPIVQHRPMLERI 180
 DB 250 ACIGGPPNCLDRLENWITS LAESQLQTRQIKLEELQKQVSKYKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGQVFTTKVRLLVKPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGQVFTTKVRLLVKPEL 358

RESULT 11

AAE22054
 ID AAE22054 standard; protein; 769 AA.

AC AAE22054;

DT 25-JUL-2002 (first entry)

DE Human Stat3 protein.

KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

XX Homo sapiens.

OS WO200220032-A1.

PN 14-MAR-2002.

PD 10-SEP-2001; 2001WO-US028254.

PF 08-SEP-2000; 2000US-0231212P.

PR (UYJO) UNIV JOHNS HOPKINS.

PA (UYSF-) UNIV SOUTH FLORIDA.

XX Yu H, Pardoll D, Jove R, Dalton W;

XX

DR WPI; 2002-362218/39.

XX N-PSDB; AAD35065.

XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.

XX Disclosure; Page 83-85; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g. bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein

XX Sequence 769 AA;

Query Match 98.7%; Score 1157; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 7.8e-98;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDARKVRVDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDARKVRVDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDELDADWKRPEI 120
 DB 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDELDADWKRPEI 249

QY 121 ACIGGPPNCLDRLENWITS LAESQLQTRQIKLEELQKQVSKYKGDPIVQHRPMLERI 180
 DB 250 ACIGGPPNCLDRLENWITS LAESQLQTRQIKLEELQKQVSKYKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGQVFTTKVRLLVKPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGQVFTTKVRLLVKPEL 358

RESULT 12

AAE22056
 ID AAE22056 standard; protein; 769 AA.

XX AC AAE22056;

XX 25-JUL-2002 (first entry)

XX Human protein related to angiogenesis regulation.

XX

KW Human; signal transducer and activator of transcription 3; ischaemia;
KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
KW shock; chronic active hepatitis; emphysema; trauma; scleroderma;
KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
KW cirrhosis; hypoproliferative disorder; lesion.
XX Homo sapiens.
XX WO200220032-A1.
XX 14-MAR-2002.
XX 10-SEP-2001; 2001WO-US028254.
XX 08-SEP-2000; 2000US-0231212P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX (UYSF-) UNIV SOUTH FLORIDA.
XX Yu H, Pardoll D, Jove R, Dalton W;
XX WPI; 2002-362218/39.
XX
XX Modulating angiogenesis and an immune response in an individual, for
XX treating a hypoxic or ischemic condition, comprises administering a
XX compound that modulates the activity of a signal transducer and activator
XX of transcription 3.
XX
XX Disclosure; Page 83-85; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
XX response. Method involves administering to an individual a compound that
XX modulate the activity of signal transducer and activator of transcription
XX 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
XX hypoxic or ischaemic condition or disorder which is the result of stroke,
XX ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
XX tissue ischaemia in the lower extremities, infarction, trauma, vascular
XX occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
XX chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
XX epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
XX nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
XX with neovascularisation. Suppressing an immune response is useful for
XX ameliorating a symptom of an autoimmune disease such as systemic lupus
XX erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
XX Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
XX mixed connective tissue disease, primary biliary cirrhosis, pernicious
XX anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
XX gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
XX idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
XX disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
XX infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
XX dense deposit disease. The method is useful in preventing or treating
XX specific proliferative and oncogenic disease which includes sarcoma and
XX carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
XX fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
XX hypoproliferative disorders, physical trauma, lesions and wounds. The
XX method is also used in gene therapy. The present sequence is human
XX protein related to angiogenesis regulation

XX SQ Sequence 769 AA;
Query Match 98.7%; Score 1157; DB 5; Length 769;
Best Local Similarity 98.7%; Pred. No. 7.8e-98;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60

Db 130 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDQRRSIVSELQGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKMOQLEQMLTALDQRRSIVSELQGLLSAMEYVQKTLTDEELADWKRQOI 249
QY 121 ACIGGPNICLDRLENNWITSLAESQLOTRQOIKKLELOQKYSYKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLENNWITSLAESQLOTRQOIKKLELOQKYSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCWMPHDPRLVIKTVQFTTKVRLVVKPEL 229
Db 310 VELFRNLMSAFVVERQPCWMPHDPRLVIKTVQFTTKVRLVVKPEL 358

RESULT 13
AAR82995
ID AAR82995 standard; protein; 770 AA.
XX
AC AAR82995;
XX
DT 25-MAR-1996 (first entry)
XX
DE Mouse liver acute phase response factor.
XX
KW Mouse; acute phase response factor; transcription factor; interleukin-6;
KW signal transduction; liver; antibody; antisense; ribozyme;
KW antiinflammatory; antitumor; hypotensive; therapy.
XX
OS Mus musculus.
XX
PN EP676469-A2.
XX
PD 11-OCT-1995.
XX
PF 29-MAR-1995; 95BP-00104670.
XX
PR 04-APR-1994; 94JP-00065825.
XX
PA (KISH/) KISHIMOTO T.
XX
PI Akira S, Kishimoto T;
XX WPI; 1995-346089/45.
DR N-PSDB; AAT05619.
XX
PT New acute phase response factor - for developing inhibitory agents for
PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
PT diseases.
XX
PS Claim 10; Page 20-22; 31pp; English.
XX
CC The sequence represents a mouse acute phase response factor (APRF), a
CC transcription factor related to signal transduction of interleukin-6 (IL-
CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
CC library using a polymerase chain reaction product (amplified using
CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
CC inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
CC hypertension, etc
XX
SQ Sequence 770 AA;

Query Match 98.7%; Score 1157; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 7.8e-98;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
Db 130 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189

QY 61 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI 249
QY 121 ACIGGPNICLDRLENWITSLEASQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLLEERI 180
DB 250 ACIGGPNICLDRLENWITSLEASQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLLEERI 309
QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVIKTGVQFTTKVRLLVKPPPEL 229
DB 310 VELFRNLMSAFVVERQPCMPHPDRPLVIKTGVQFTTKVRLLVKPPPEL 358

RESULT 14

AA03768
ID AAY03768 standard; protein; 770 AA.

XX
AC AAY03768;

DT 11-JUN-1999 (first entry)

DE Human STAT3 allelic variant.

KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
KW intracellular transcription factor; interleukin-6; medicament; variant;
KW pharmaceutical; autoimmune disease; inflammatory; human.

OS Homo sapiens.

PN EP905234-A2.

XX 31-MAR-1999.

XX 18-FEB-1998; 98EP-00102774.

XX 16-SEP-1997; 97EP-00116061.

XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PA Serlupi-Crescenzi O, Della Pietra L;

XX WPI; 1999-192664/17.

DR N-PSDB; AAX29281.

PT New human Signal Transducer and Activator of Transcription 3 (STAT3)
PT allelic variant useful for treatment of autoimmune and inflammatory
PT disease.

XX Claim 2; Page 9-13; 32pp; English.

XX The present sequence represents a predominant allelic variant of human
CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
CC intracellular transcription factor which mediates IL-6 signals. The
CC encoding sequence differs from the original published human STAT3 gene
CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
CC DNA molecule can be used for the recombinant expression of the variant.
CC STAT3 protein is useful as a medicament or pharmaceutical composition for
CC treatment of autoimmune or inflammatory diseases

XX Sequence 770 AA;

SQ Query Match 98.7%; Score 1157; DB 2; Length 770;

Best Local Similarity 98.7%; Pred. NO. 7.8e-98;

Matches 256; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEBQHLQDARKVRQDLERQKMKVVENLQDDPFDNYKTLKSGQDMQDLN 60

DB 130 NHPTAAVTEKQOMLEBQHLQDARKVRQDLERQKMKVVENLQDDPFDNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

DB 190 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI 249

QY 121 ACIGGPNICLDRLENWITSLEASQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLLEERI 180
DB 250 ACIGGPNICLDRLENWITSLEASQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLLEERI 309
QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVIKTGVQFTTKVRLLVKPPPEL 229
DB 310 VELFRNLMSAFVVERQPCMPHPDRPLVIKTGVQFTTKVRLLVKPPPEL 358

RESULT 15

AA012377

ID AAB12377 standard; peptide; 770 AA.

XX
AC AAB12377;

XX 08-NOV-2000 (first entry)

XX N-terminal domain of murine STAT-3 protein.

XX STAT; signal transducer and activator of transcription; crystal;
KW drug design; murine.

XX Mus sp.

XX Key Location/Qualifiers

FT Region 4..9

FT /label= Alpha helix 1

FT Region 12..21

FT /label= Alpha helix 2

FT Region 19..21

FT /label= 3(10) helix of alpha helix 2

FT Region 28..33

FT /label= Alpha helix 3

FT Region 35..40

FT /label= Alpha helix 4

FT Region 43..47

FT /label= Alpha helix 5

FT Region 50..73

FT /label= Alpha helix 6

FT Region 77..96

FT /label= Alpha helix 7

FT Region 99..119

FT /label= Alpha helix 8

XX US6087478-A.

PN 11-JUL-2000.

XX 23-JAN-1998; 98US-00012710.

XX 23-JAN-1998; 98US-00012710.

XX (UYRQ) UNIV ROCKEFELLER.

XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;

XX WPI; 2000-505108/45.

XX New crystals of an N-terminal fragment of a signal transducer and

XX activator of transcription that effectively diffracts x-rays, useful for

XX drug screening and development.

XX Disclosure; Fig 1; 42pp; English.

XX The present invention relates to a crystal of an N-terminal fragment of a
CC signal transducer and activator of transcription (STAT) protein. The
CC crystal effectively diffracts X-rays, allowing the determination of the
CC atomic coordinates of the N-terminal domain to a resolution of greater
CC than 5.0 Angstroms. The present sequence is the N-terminal domain of the
CC murine STAT3 protein. The N-terminal domain enables STAT dimers to
CC interact and bind DNA cooperatively, a mechanism important for gene
CC activation. The crystals are useful in drug screening and development by
CC selecting a potential drug by performing rational drug design with the 3-

CC dimensional structure determined for the crystal

XX
SQ Sequence 770 AA;

Query Match 98.7%; Score 1157; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 7.8e-98;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	NHPTAAVTEKQQLLEQHLQDARKVQDLLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN	60
Db	130	NHPTAAVTEKQQLLEQHLQDARKVQDLLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN	189
Qy	61	GNNQSVTRQKMQQLLEQMLTALDQWRSIVSELGILLSAMEYVQKTLTDEELADWKRPEI	120
Db	190	GNNQSVTRQKMQQLLEQMLTALDQWRSIVSELGILLSAMEYVQKTLTDEELADWKRQOI	249
Qy	121	ACIGPPNICLDRLNNWITSIAESQLQTRQIKLELQKQVSYKGDPIVQHRPMLLEERI	180
Db	250	ACIGPPNICLDRLNNWITSIAESQLQTRQIKLELQKQVSYKGDPIVQHRPMLLEERI	309
Qy	181	VELFRNLKSAFVVERQPCMPMHDPRLVITGVQFTTKVRLLLVKFPEL	229
Db	310	VELFRNLKSAFVVERQPCMPMHDPRLVITGVQFTTKVRLLLVKFPEL	358

Search completed: May 25, 2005, 17:36:39
Job time : 123.057 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 28.6534 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-31
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQVFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1172	100.0	229	3	US-09-387-418A-31
2	1168	99.7	229	3	US-09-387-418A-18
3	1168	99.7	229	3	US-09-387-418A-28
4	1168	99.7	252	3	US-09-387-418A-14
5	1168	99.7	271	3	US-09-387-418A-9
6	1168	99.7	770	1	US-08-369-796-12
7	1168	99.7	770	2	US-08-852-091-12
8	1168	99.7	770	2	US-08-820-754-12
9	1168	99.7	770	3	US-08-956-652-12
10	1168	99.7	770	3	US-08-869-869-12
11	1168	99.7	770	3	US-08-948-547-12
12	1168	99.7	770	3	US-09-364-970-3
13	1168	99.7	770	3	US-09-364-970-5
14	1168	99.7	770	3	US-08-956-653A-12
15	1168	99.7	770	4	US-08-212-185-12
16	1168	99.7	770	5	PCT-US95-17025-12
17	1163	99.2	229	3	US-09-387-418A-30
18	1157	98.7	770	1	US-08-416-581B-9
19	1157	98.7	770	3	US-09-012-710-8
20	1157	98.7	770	3	US-09-556-273-8
21	1157	98.7	770	3	US-09-526-542-2
22	1157	98.7	770	4	US-10-117-087-2
23	1152	98.3	770	1	US-08-416-581B-1
24	1152	98.3	770	1	US-08-416-581B-5
25	1152	98.3	770	3	US-09-087-465-6
26	1152	98.3	770	4	US-09-972-800A-6
27	1152	98.3	771	1	US-08-276-099A-14

28	1152	98.3	771	1	US-08-781-890-14	Sequence 14, Appl
29	1151	98.2	229	3	US-09-387-418A-29	Sequence 29, Appl
30	1090	93.0	213	3	US-09-387-418A-19	Sequence 19, Appl
31	1090	93.0	236	3	US-09-387-418A-15	Sequence 15, Appl
32	1044	89.1	223	3	US-09-387-418A-22	Sequence 22, Appl
33	845	72.1	185	3	US-09-387-418A-23	Sequence 23, Appl
34	777	66.3	176	3	US-09-387-418A-16	Sequence 16, Appl
35	653	55.7	128	3	US-09-387-418A-20	Sequence 20, Appl
36	601	51.3	143	3	US-09-387-418A-17	Sequence 17, Appl
37	571	48.7	129	3	US-09-387-418A-24	Sequence 24, Appl
38	569	48.5	268	4	US-09-387-418A-12	Sequence 12, Appl
39	569	48.5	582	4	US-09-430-806A-3	Sequence 3, Appl
40	569	48.5	712	1	US-08-369-796-6	Sequence 6, Appl
41	569	48.5	712	2	US-08-852-091-6	Sequence 6, Appl
42	569	48.5	712	2	US-08-820-754-6	Sequence 6, Appl
43	569	48.5	712	3	US-08-956-652-6	Sequence 6, Appl
44	569	48.5	712	3	US-08-956-869-6	Sequence 6, Appl
45	569	48.5	712	3	US-08-948-547-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-387-418A-31
; Sequence 31, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-387-418A-31

Query Match	100.0%	Score 1172;	DB 3;	Length 229;
Best Local Similarity	100.0%	Pred No. 2.7e-99;	Mismatches 0;	Indels 0; Gaps 0;
Matches 229;	Conservative 0;			
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Db	1	NHPTAAVTEKQOMLEQHLQDARKRVODLEQKMVVENLQDDPFFNYKTLKSGQDMQDLN	60	
Qy	61	GNNQSVTRQMKQOQLEQMLTALQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI	120	
Db	61	GNNQSVTRQMKQOQLEQMLTALQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI	120	
Qy	121	ACIGGPNICLDRLENIWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI	180	
Db	121	ACIGGPNICLDRLENIWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI	180	
Qy	181	VELFRNLMSAFVVERQPCMPHPRPLVIKTGVQFTTKVRLLVKFPPEL	229	
Db	181	VELFRNLMSAFVVERQPCMPHPRPLVIKTGVQFTTKVRLLVKFPPEL	229	

RESULT 2
US-09-387-418A-18
; Sequence 18, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H

```

; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-18

Query Match          99.7%; Score 1168; DB 3; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.3e-99;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQMKVVENLQDDFDFNYKTLKSQGDMDQLN 60
Qy 61 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRPEI 120
Qy 121 ACITGGPPNICLDRLNNWITSLAESOLOTRQOIKKLEELQOKSVYKGDPIVOHRPMLERI 180
Db 121 ACITGGPPNICLDRLNNWITSLAESOLOTRQOIKKLEELQOKSVYKGDPIVOHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPMHDPDRPLVIKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPMHDPDRPLVIKTGVQFTTKVRLLVKFPPEL 229

RESULT 3
US-09-387-418A-28
; Sequence 28, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-28

Query Match          99.7%; Score 1168; DB 3; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.3e-99;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTEKQOMLEQHLQDARKRVQDLEQMKVVENLQDDFDFNYKTLKSQGDMDQLN 60
Db 1 NHPTAAVVTEKQOMLEQHLQDVRKRVQDLEQMKVVENLQDDFDFNYKTLKSQGDMDQLN 60
Qy 61 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQMKQOMLEQMLTALDQMRRSIVSELAGILSAMEYVQKTLTDEELADWKRPEI 120
Qy 121 ACITGGPPNICLDRLNNWITSLAESOLOTRQOIKKLEELQOKSVYKGDPIVOHRPMLERI 180
Db 121 ACITGGPPNICLDRLNNWITSLAESOLOTRQOIKKLEELQOKSVYKGDPIVOHRPMLERI 180

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Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
 DB 24 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 83
 QY 61 GNNQSVTRQMKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 120
 DB 84 GNNQSVTRQMKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 143
 QY 121 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 180
 DB 144 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 203
 QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVQFTTKVRLLVKPEL 229
 DB 204 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVQFTTKVRLLVKPEL 252

RESULT 6
 US-08-369-796-12
 ; Sequence 12, Application US/08369796
 ; Patent No. 5716622
 ; GENERAL INFORMATION:
 ; APPLICANT: James E. Darnell, Jr.
 ; APPLICANT: Zilong Wen
 ; APPLICANT: Curt M. Horvath
 ; APPLICANT: Zhong Zhong
 ; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 ; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/369,796
 ; FILING DATE: 06-JAN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-369-796-12

Query Match 99.7%; Score 1168; DB 1; Length 770;
 Best Local Similarity 99.6%; Pred. No. 3e-98;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
 DB 130 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 189
 QY 61 GNNQSVTRQMKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 120

DB 190 GNNQSVTRQMKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 249
 QY 121 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 180
 DB 250 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 309
 QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVQFTTKVRLLVKPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVQFTTKVRLLVKPEL 358

RESULT 7
 US-08-852-091-12
 ; Sequence 12, Application US/08852091
 ; Patent No. 5883228
 ; GENERAL INFORMATION:
 ; APPLICANT: James E. Darnell, Jr.
 ; APPLICANT: Zilong Wen
 ; APPLICANT: Curt M. Horvath
 ; APPLICANT: Zhong Zhong
 ; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 ; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/852,091
 ; FILING DATE: 06-MAY-1997
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/369,796
 ; FILING DATE: 06-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-852-091-12

Query Match 99.7%; Score 1168; DB 2; Length 770;
 Best Local Similarity 99.6%; Pred. No. 3e-98;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
 DB 130 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 189
 QY 61 GNNQSVTRQMKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 120
 DB 190 GNNQSVTRQMKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 249
 QY 121 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 180
 DB 250 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 309

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Qy   181 VELFRNLKSAFVVERPCMPMHDPDRPLVIKTGVQFTTKVRLLVKFPPEL 229
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Db   310 VELFRNLKSAFVVERPCMPMHDPDRPLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 8
US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent NO. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,754
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-754-12

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Qy 61 GNNQSVTRQMQOQLBQMLTALDQWRRSIVSSELAGLISAMEYVQKTLTDEELADWKRRPEI 249
Db 190 GNNQSVTRQMQOQLBQMLTALDQWRRSIVSSELAGLISAMEYVQKTLTDEELADWKRRPEI 249
Qy 121 ACIGPPNCLDLRLENWITSLAESQLQTRQIKKLELQOKVSYKGDPIVQHRPMLLEERI 180
Db 250 ACIGPPNCLDLRLENWITSLAESQLQTRQIKKLELQOKVSYKGDPIVQHRPMLLEERI 309
Qy 181 VELFRNLKMSAFVVERQPCMPMHDPDRPLVINKTVGVQFTTKVRLLLVKPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPMHDPDRPLVINKTVGVQFTTKVRLLLVKPPEL 358

RESULT 9
US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,652
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-652-12

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Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches: 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTBKQMLEQHLQDARXRVQDLEQKMKVVENLQDDFDFNYKTLKSKQGDMDLN 60
Db 130 NHPTAAVVTBKQMLEQHLQDARXRVQDLEQKMKVVENLQDDFDFNYKTLKSKQGDMDLN 189

Qy 61 GNNQSVTRQKMQQLEQMLTALDQWRRSIVSELAGLLSAMESVYQKTLTDEELADWKRRPEI 120
Db 190 GNNQSVTRQKMQQLEQMLTALDQWRRSIVSELAGLLSAMESVYQKTLTDEELADWKRRPEI 249

Qy 121 ACICGPPNICLDRLENWITSLSAQSLOTQROQIKKLEELQKSVYKGDPIVOHRPMLERI 180
Db 250 ACICGPPNICLDRLENWITSLSAQSLOTQROQIKKLEELQKSVYKGDPIVOHRPMLERI 309

Qy 181 VELFRNLKSAFVVERPCPMHPDRPLVIKTVGQFTTKVRLLVKFPPEL 229
Db 310 VELFRNLKSAFVVERPCPMHPDRPLVIKTVGQFTTKVRLLVKFPPEL 358

RESULT 10
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schnelller, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match          99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRKYQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDVERKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 189

QY 61 GNNQSVTRQKMQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB 190 GNNQSVTRQKMQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 249

QY 121 ACTGGPPNICLDRLNWTSLAESQLQTRQIIKKLELOOKVSYKGDPIVQHRPMLREI 180
DB 250 ACTGGPPNICLDRLNWTSLAESQLQTRQIIKKLELOOKVSYKGDPIVQHRPMLREI 309

QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVIKTGVQFTTKVRLVVKPEL 229
DB 310 VELFRNLMSAFVVERQPCMPHPDRPLVIKTGVQFTTKVRLVVKPEL 358

RESULT 11
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match          99.7%; Score 1168; DB 3;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1;

QY 1 NHPTAAVTEKQOMLEQHQLQDARKKRVQDLEQRMKVVENLQ
DB 130 NHPTAAVTEKQOMLEQHQLQDVRKRVQDLEQRMKVVENLQ
QY 61 GNNQSVTRQMKQOOLEQMLTALDQRRRSIVSELAGLLSAME
DB 190 GNNQSVTRQMKQOOLEQMLTALDQRRRSIVSELAGLLSAME
QY 121 ACTGGPPNCLDPLENNWITSLAESQLQTRQOQIKKLEEQO
DB 250 ACTGGPPNCLDRLNNWITSLAESQLQTRQOQIKKLEEQO
QY 181 VELFRNLMSAFVVERQPCWMPHPDRPLVIKTVGVQFTTKV
DB 310 VELFRNLMSAFVVERQPCWMPHPDRPLVIKTVGVQFTTKV

RESULT 11
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 130 NHPTAAVVTKEQQLLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
QY 61 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLNNITSLAESQLTRQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNNITSLAESQLTRQIKKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 12
US-09-364-970-3
Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-3

Query Match 99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 130 NHPTAAVVTKEQQLLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
QY 61 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLNNITSLAESQLTRQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNNITSLAESQLTRQIKKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 13
US-09-364-970-5
Sequence 5, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-5

Query Match 99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 130 NHPTAAVVTKEQQLLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
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DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLNNITSLAESQLTRQIKKLEELQKVS YKGDPIVQHRPMLERI 180
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RESULT 14
US-08-956-653A-12
Sequence 12, Application US/08956653A
Patent No. 6338949
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/212,185
APPLICATION NUMBER: 11-MAR-1994
FILING DATE:

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; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-653A-12

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Query Match          99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 190 GNNQSVTRQKMOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
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QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
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RESULT 15
US-08-212-185-12
; Sequence 12, Application US/08212185
; Patent No. 6605442
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-212-185-12

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Query Match          99.7%; Score 1168; DB 4; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 130 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGDMQDLN 189
QY 61 GNNQSVTRQKMOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMOQLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
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QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: May 25, 2005, 17:36:58 ; Search time 100.287 Seconds
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Title: US-10-090-185-31
Perfect score: 1172
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Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1168	99.7	229	13	US-10-090-185-28
4	1168	99.7	252	13	US-10-090-185-14
5	1168	99.7	271	13	US-10-090-185-9
6	1168	99.7	770	11	US-09-876-773-12
7	1168	99.7	770	17	US-10-639-617-12
8	1163	99.2	229	13	US-10-090-185-30
9	1157	98.7	720	15	US-10-380-020-4
10	1157	98.7	769	15	US-10-380-020-2
11	1157	98.7	769	15	US-10-380-020-5
12	1157	98.7	770	14	US-10-045-792-8
13	1157	98.7	770	14	US-10-038-010-56

14	1157	98.7	770	14	US-10-117-087-2	Sequence 2, Appli
15	1157	98.7	793	9	US-09-925-302-780	Sequence 780, App
16	1157	98.7	793	10	US-09-925-302-780	Sequence 780, App
17	1154	98.5	770	15	US-10-116-275-329	Sequence 329, App
18	1152	98.3	770	15	US-10-116-275-349	Sequence 349, App
19	1151	98.2	229	13	US-10-090-185-29	Sequence 29, Appli
20	1090	93.0	213	13	US-10-090-185-19	Sequence 19, Appli
21	1090	93.0	236	13	US-10-090-185-15	Sequence 15, Appli
22	1044	89.1	223	13	US-10-090-185-22	Sequence 22, Appli
23	845	72.1	185	13	US-10-090-185-23	Sequence 23, Appli
24	777	66.3	176	13	US-10-090-185-16	Sequence 16, Appli
25	653	55.7	128	13	US-10-090-185-20	Sequence 20, Appli
26	601	51.3	143	13	US-10-090-185-17	Sequence 17, Appli
27	573	48.9	749	9	US-09-833-205-4	Sequence 4, Appli
28	571	48.7	129	13	US-10-090-185-24	Sequence 24, Appli
29	569	48.5	268	13	US-10-090-185-12	Sequence 12, Appli
30	569	48.5	582	14	US-10-245-120-3	Sequence 3, Appli
31	569	48.5	712	11	US-09-876-773-6	Sequence 6, Appli
32	569	48.5	712	14	US-10-245-120-2	Sequence 2, Appli
33	569	48.5	712	17	US-10-639-617-6	Sequence 6, Appli
34	569	48.5	712	17	US-10-936-390-5	Sequence 5, Appli
35	569	48.5	750	9	US-09-833-205-2	Sequence 2, Appli
36	569	48.5	750	11	US-09-876-773-4	Sequence 4, Appli
37	569	48.5	750	14	US-10-245-120-1	Sequence 1, Appli
38	569	48.5	750	14	US-10-308-279-44	Sequence 44, Appli
39	569	48.5	750	16	US-10-753-889-352	Sequence 352, App
40	569	48.5	750	16	US-10-755-889-823	Sequence 823, App
41	569	48.5	750	17	US-10-492-043-19	Sequence 19, Appli
42	569	48.5	750	17	US-10-639-617-4	Sequence 4, Appli
43	569	48.5	786	9	US-09-925-297-550	Sequence 550, App
44	562	48.0	749	9	US-09-833-205-6	Sequence 6, Appli
45	562	48.0	749	11	US-09-876-773-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-090-185-31
; Sequence 31, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-090-185-31

Query Match 100.0%; Score 1172; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 7.5e-95;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 GNNQSVTRQMKOQLEQMLTALDQMRRESIVSELAGLLSAMEYVQKTLTDELDADWKRPEI 120
DB 61 GNNQSVTRQMKOQLEQMLTALDQMRRESIVSELAGLLSAMEYVQKTLTDELDADWKRPEI 120

Qy	121	ACITGGPNTCLDRLENWITSLSAQLOTRQOIKKLEELQOKSVYKGDPIVOHRPMLERI	180
Db	121	ACITGGPNTCLDRLENWITSLSAQLOTRQOIKKLEELQOKSVYKGDPIVOHRPMLERI	180
Qy	181	VELFRNLKMSAFVFERQPCWMPHDPRLVIKTGVQFTTKVRLLVKFPPEL	229
Db	181	VELFRNLKMSAFVFERQPCWMPHDPRLVIKTGVQFTTKVRLLVKFPPEL	229

PRECIT.T 2

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RESULI 2
US-10-090-185-18
; Sequence 18, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR E
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: prt
; ORGANISM: Mus musculus
US-10-090-185-18

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DEPT. T. A

RESULT 4
 US-10-090-185-14
 ; Sequence 14, Application US/10090185
 ; Publication No. US20020197647A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Xiaokui
 ; APPLICANT: Wrzeszczynska, Melissa H
 ; APPLICANT: Horvath, Curt M
 ; APPLICANT: Darnell Jr., James E
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
 ; TITLE OF INVENTION: INTERACTIONS
 ; FILE REFERENCE: 600-1-253
 ; CURRENT APPLICATION NUMBER: US/10/090,185
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: 09/387,418
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 252
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-090-185-14

RESULTS. T 5

RESOL 3
US-10-090-185-9

; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
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; ORGANISM: Mus musculus
US-10-090-185-9

Query Match 99.7%; Score 1168; DB 13; Length 271;
Best Local Similarity 99.6%; Pred. No. 2,1e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq. David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 99.7%; Score 1168; DB 11; Length 770;
Best Local Similarity 99.6%; Pred. No. 7.9e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/639,617
; FILING DATE: 12-AUG-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO 99/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELE: 139521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 99.7%; Score 1168; DB 17; Length 770;
Best Local Similarity 99.6%; Pred. No. 7.9e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGPPNICLDRLENWITSLSAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLSAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 358

RESULT 8
US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229

; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-30

Query Match 99.2%; Score 1163; DB 13; Length 229;
Best Local Similarity 99.1%; Pred. No. 4.6e-94;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
QY 121 ACIGPPNICLDRLENWITSLSAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 180
DB 121 ACIGPPNICLDRLENWITSLSAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 180
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 229

RESULT 9
US-10-380-020-4
; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match 98.7%; Score 1157; DB 15; Length 720;
Best Local Similarity 98.7%; Pred. No. 6.7e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGPPNICLDRLENWITSLSAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLSAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 358

RESULT 10
US-10-380-020-2
; Sequence 2, Application US/10380020
; Publication No. US20040052762A1

QY 121 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKSVYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 13

US-10-038-010-56
 ; Sequence 56, Application US/10038010
 ; Publication No. US20030040089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYBRIGENICS
 ; APPLICANT: Pierre, Legrain
 ; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
 ; FILE REFERENCE: B4767A
 ; CURRENT APPLICATION NUMBER: US/10/038,010
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 60/259,377
 ; PRIOR FILING DATE: 2001-01-02
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 56
 ; LENGTH: 770
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: STAT3 : Transcription factor
 ; LOCATION: (1)..(770)
 ; OTHER INFORMATION:
 US-10-038-010-56

Query Match 98.7%; Score 1157; DB 14; Length 770;
 Best Local Similarity 98.7%; Pred. No. 7.3e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60
 Db 130 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQI 249
 QY 121 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKSVYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 14

US-10-117-087-2
 ; Sequence 2, Application US/10117087
 ; Publication No. US20030166854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SERLUP1-CRESCENZI, Ottaviano
 ; APPLICANT: DELIA PIETRA, Linda
 ; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
 ; FILE REFERENCE: SERLUP1-2
 ; CURRENT APPLICATION NUMBER: US/10/117,087
 ; CURRENT FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: US/09/526,542
 ; PRIOR FILING DATE: 2000-03-19
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 770
 ; TYPE: PRT

; ORGANISM: Human
 US-10-117-087-2
 Query Match 98.7%; Score 1157; DB 14; Length 770;
 Best Local Similarity 98.7%; Pred. No. 7.3e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60
 Db 130 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQI 249
 QY 121 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKSVYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 15

US-09-925-302-780
 ; Sequence 780, Application US/09925302
 ; Patent No. US20020044941A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA104
 ; CURRENT APPLICATION NUMBER: US/09/925,302
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05918
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 896
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 780
 ; LENGTH: 793
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-302-780

Query Match 98.7%; Score 1157; DB 9; Length 793;
 Best Local Similarity 98.7%; Pred. No. 7.6e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60
 Db 153 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 212
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 213 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQI 272
 QY 121 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKSVYKGDPIVQHRPMLERI 180
 Db 273 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKSVYKGDPIVQHRPMLERI 332
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
 Db 333 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 381

Search completed: May 25, 2005, 18:21:55
 Job time : 101.62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-31
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQVFTKVRLLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1157	98.7	770	2 I49508	ISGF3 p91-related
2	1152	98.3	770	2 A54444	DNA-binding protei
3	523.5	44.7	739	2 A46159	interferon-depende
4	508	43.3	748	2 A56047	gamma-interferon a
5	322	27.5	851	2 A46160	interferon alpha-i
6	268.5	22.9	786	2 I49274	mammary gland fact
7	268.5	22.9	793	2 S54772	mammary gland fact
8	262.5	22.4	794	2 G02317	transcription acti
9	237	20.2	794	2 S55527	mammary gland fact
10	127	10.8	848	2 A54740	interleukin-4-indu
11	125.5	10.7	837	2 I57557	DNA-Binding Protei
12	122.5	10.5	1208	2 AE1947	chromosome segrega
13	122	10.4	533	2 G72593	hypothetical prote
14	122	10.4	978	2 A70387	conserved hypothet
15	120.5	10.3	1166	2 T27075	hypothetical prote
16	116.5	9.9	1509	1 A27224	myosin heavy chain
17	116.5	9.9	2094	2 S33124	tpy protein - huma
18	114.5	9.8	284	2 C64527	M protein - Helico
19	114.5	9.8	857	2 S33821	median body protei
20	113.5	9.7	924	2 S06117	myosin heavy chain
21	113	9.6	1999	1 S21801	myosin heavy chain
22	112.5	9.6	1690	2 T13030	microtubule bindin
23	112.5	9.6	2007	1 B43402	myosin heavy chain
24	112.5	9.6	2253	2 T30336	nuclear/mitotic ap
25	112	9.6	289	2 S51193	epimorphin - mouse
26	112	9.6	1976	2 A59252	myosin heavy chain
27	111	9.5	284	2 S24401	tropomyosin 2, ske
28	111	9.5	734	2 T27055	hypothetical prote
29	111	9.5	853	2 T51505	hypothetical prote

30	111	9.5	1164	2 T24806	hypothetical prote
31	111	9.5	1188	2 G83960	chromosome segrega
32	110.5	9.4	1738	2 T14867	interaptin - slime
33	109.5	9.3	434	2 T43448	hypothetical prote
34	109.5	9.3	464	2 H90279	microtubule bindin
35	109.5	9.3	727	2 AC1814	hypothetical prote
36	109.5	9.3	1048	1 BVSCSC	exonuclease (EC 3.
37	109.5	9.3	1957	2 T38077	hypothetical coile
38	109.5	9.3	2442	2 T08621	centrosome associa
39	109	9.3	1959	1 A33977	myosin heavy chain
40	109	9.3	3187	2 JCS837	364K Golgi complex
41	108.5	9.3	946	2 S28061	SCP1 protein - rat
42	108.5	9.3	1940	2 A59287	myosin heavy chain
43	108.5	9.3	1392	2 A47297	myosin heavy chain
44	108	9.2	2677	2 A38194	desmoplakin 1 - hu
45	107.5	9.2	527	2 S33068	myosin heavy chain

ALIGNMENTS

RESULT 1

I49508
ISGF3 p91-related transcription factor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49508; I49009
R:Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A:Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr
A:Reference number: A54444; MUID:94208062; PMID:7512451
A:Accession: I49508
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-770 <RES>
A:Cross-references: UNIPROT:P42227; GB:I29278; NID:9476715; PIDN:AAA37254.1; PID:947671
R:Kaz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
A:Title: Acute phase response factor and additional members of the interferon-stimulate
A:Reference number: I49009; MUID:95014185; PMID:7523373
A:Accession: I49009
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-393, 'M', 395-700, 702-770 <RE2>
A:Cross-references: EMBL:U08378; NID:9473889; PIDN:AAA56668.1; PID:9473890
C:Genetics:
A:Gene: APRE
C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match	98.7%	Score 1157;	DB 2;	Length 770;
Best Local Similarity	98.7%;	Pred. No. 2.7e-69;		
Matches 226;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	NHPTAAVTEKQOMLEQHLQDARKVQDLQKQKVENLQDDPDNFKYTKLSQGDMDLN	60	
Db	130	NHPTAAVTEKQOMLEQHLQDARKVQDLQKQKVENLQDDPDNFKYTKLSQGDMDLN	189	
QY	61	GNQSVTRQKMOQLQMLTALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI	120	
Db	190	GNQSVTRQKMOQLQMLTALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI	249	
QY	121	ACIGPPNICLDRLNWTSLAESQLQTRQIQIKLELQKQKSYKGDPTVQHRPMLERI	180	
Db	250	ACIGPPNICLDRLNWTSLAESQLQTRQIQIKLELQKQKSYKGDPTVQHRPMLERI	309	
QY	181	VELFNLKMSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKPEL	229	
Db	310	VELFNLKMSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKPEL	358	

RESULT 2
A54444
DNA-binding protein APRF - human

C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A54444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
C;Genetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
A;Title: A novel gamma interferon activation site-binding protein expressed in e
A;Reference number: A56047; MUID:94277038; PMID:8007943
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor

Query Match 98.3%; Score 1152; DB 2; Length 770;
Best Local Similarity 98.3%; Pred. No. 5.9e-69;
Matches 225; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 130 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189

QY 61 GNNQSVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKLTDEELADWKRQOI 249

QY 121 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELQKVSXKGGPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELQKVSXKGGPIVQHRPMLERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 44.7%; Score 523.5; DB 2; Length 739;
Best Local Similarity 45.8%; Pred. No. 2.6e-27;
Matches 103; Conservative 49; Mismatches 60; Indels 13; Gaps 2;

QY 5 AAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNQ 64
DB 132 STVMDLKQELDSKRVNRKQKMCIEHEIKSLDLDQYDFKCKTL--QNRHETNGVAK 189

QY 65 SVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKLTDEELADWKRPEIACIG 124
DB 190 SDQKQEQLLKQMYLMDNKRKEVWHKI IELLNVTELTQNALINDELVEKRRQSQACIG 249

QY 125 GPNICLDRLNWTSLAESQLTROQIKKLELQKVSXKGGPIVQHRPMLERIVELF 184
DB 250 GPNICLDRLNWTSLAESQLTROQIKKLELQKVSXKGGPIVQHRPMLERIVELF 309

DB 250 GPNACLDLQ-----QVRQQLKKLELEQKYTVEHDPITKNKQVLWDRTFSLF 298

QY 185 RNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 299 QQLIOSFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKQEL 343

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins
Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:g509502; PID:AAA19692.1; PID:g50950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 43.3%; Score 508; DB 2; Length 748;
Best Local Similarity 45.5%; Pred. No. 2.8e-26;
Matches 102; Conservative 48; Mismatches 66; Indels 8; Gaps 2;

QY 8 VTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKS--QGDMDLNGNQ 65
DB 136 VSEQRNVHEKVSIAKNSVQMTQDPTKYLELDQDFDYKTIQTWDQGD-----KNSI 189

QY 66 VTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKLTDEELADWKRPEIACIG 125
DB 190 LVNQEVLTQELMNSLDFKKEALSQVITVNETDLNMSMLEELQDWKRRQOIACIG 249

QY 126 PPNICLDRLNWTSLAESQLTROQIKKLELQKVSXKGGPIVQHRPMLERIVELF 185
DB 250 PLHGLDQQLQNCFTLLAESLFQLRQLEKQKQSTQMTYEGDPIPAQRAHLLETRATFLY 309

QY 186 NLMKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 NLFKNSFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 353

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
N;Alternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-851 <FU>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
submitted to the EMBL data library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:gl293919; PID:AAA98760.1; PID:gl293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in

A:Reference number: S53873; MUID:95192056; PMID:7885841

A:Accession: S53873

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-196;392-591;684-730 <YAW>

A:Cross-references: EMBL:U18671

C:Genetics:

A:Gene: stat2

A:Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 40/2

C:Superfamily: human signal transducer and transcription activator STAT5A

C:Keywords: signal transduction; transcription regulation

Query Match 27.5%; Score 322; DB 2; Length 851;

Best Local Similarity 33.5%; Pred. No. 6.9e-14;

Matches 74; Conservative 51; Mismatches 90; Indels 6; Gaps 4;

QY 8 VTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGQMDLNGNNSVT 67

DB 138 VESQHEIESRILDLRAMWEKLVKISQLKDQDVCFRYK-IOAKGKTPSLDPH--QTK 194

QY 68 RQKMOOLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEIACGGPP 127

DB 195 EQKI--LQETNELDKRRKEVLDAKALLGLRTLTIELLL-PKLEWKAQQKACIRAPI 251

QY 128 NICLDLENWITSLAESQLOTRQOIKKLELOQKVSQKDPVQHRPMLERIVELFRNL 187

DB 252 DHGLEQLWFTAGAKLLFHLRQLLKSLGSLVSYDDPLTKGVDLRNAQVTELLQRL 311

QY 188 MKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVAVKPE 228

DB 312 LHRFAFVETQPCMPQTPHRLPLIKTGSKFTVTRLLVRLQE 352

RESULT 6

I49274

mammary gland factor - mouse

N:Alternate names: STAT5 protein homolog p80

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49274; S54773; S54727

R:Liou, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in

A:Reference number: I49273; MUID:96004632; PMID:7568026

A:Accession: I49274

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-786 <RES>

A:Cross-references: UNIPROT:P42232; UNIPROT:Q9JUM1; EMBL:U21110; NID:g747973; PIDN:AA052

R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A:Reference number: S54772; MUID:95237198; PMID:7720707

A:Accession: S54773

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-432, 'E', 434-786 <MUI>

A:Cross-references: EMBL:248539; NID:g758635; PIDN:CAA8420.1; PID:g758636

R:Azam, M.; Erdjument-Bronage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,

EMBO J. 14, 1402-1411, 1995

A:Title: Interleukin-3 signals through multiple isoforms of Stat5.

A:Reference number: S54725; MUID:95246733; PMID:7537213

A:Accession: S54727

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-432, 'E', 434-786 <AZA>

C:Genetics:

A:Gene: Stat5b

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.9%; Score 268.5; DB 2; Length 786;

Best Local Similarity 30.6%; Pred. No. 2.2e-10;

Matches 71; Conservative 41; Mismatches 99; Indels 21; Gaps 5;

transcription activator stat5a - human

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 09-Jul-2004

QY 5 AAVVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNY-KTLKSGQMDLNGNN 63

DB 134 ADAMSQKHLQINQTFEELRLITQDTENELKCLQQTQVEFIQYQESLRQAOFAQLGQLN 193

QY 64 -----QSVTRQKMQOLEQML-----TALDQMRRSIVSELAGLSAMEYVQKTLTDEELA 112

DB 194 PQRMSRRTALQOKQVSLTQLQREAOQLQQRVRLAEKHQKTLQLLRKQQTILDDLELI 253

QY 113 DWKRPEIACIGPPNICLDRLNWTITSLAESOLOTRQOIKKLEELQKQVSKYKGDPIVQHR 172

DB 254 QMKRQQLAGNGGPPGSLDLVQSWCEKLAETIWNQRQIRRAEHLCCQLPIPG-PVEEM 312

QY 173 RQMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVV 224

DB 313 LAENVATITDIISALVTSTFIIEKQP-----POVLKTQTKFAATVRLVV 356

RESULT 7

S54772

mammary gland factor - mouse

N:Alternate names: stat5 protein

C:Species: Mus musculus (house mouse)

C>Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S54772; I49273

R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A:Reference number: S54772; MUID:95237198; PMID:7720707

A:Accession: S54772

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-793 <MUI>

A:Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA8

R:Liou, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved

A:Reference number: I49273; MUID:96004632; PMID:7568026

A:Accession: I49273

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-793 <RES>

A:Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972

C:Genetics:

A:Gene: Stat5a

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.9%; Score 268.5; DB 2; Length 793;

Best Local Similarity 30.6%; Pred. No. 2.2e-10;

Matches 70; Conservative 41; Mismatches 97; Indels 21; Gaps 5;

QY 8 VTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNY-KTLKSGQMDLNGNN--- 63

DB 137 MSQKHLQINQRFEEELRLITQDTENELKCLQQTQVEFIQYQESLRQAOFAQLGQLNPQE 196

QY 64 -----QSVTRQKMQOLEQML-----TALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWK 115

DB 197 RMSRRTALQOKQVSLTQLQREAOQLQQRVRLAEKHQKTLQLLRKQQTILDDLELIQWK 256

QY 116 RPETACTGPPNICLDRLNWTITSLAESOLOTRQOIKKLEELQKQVSKYKGDPIVQHRPM 175

DB 257 RRQQLAGNGGPPGSLDLVQSWCEKLAETIWNQRQIRRAEHLCCQLPIPG-PVEEMLA 315

QY 176 LEERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVV 224

DB 316 VNATITDIISALVTSTFIIEKQP-----POVLKTQTKFAATVRLVV 356

RESULT 8

G02317

transcription activator stat5a - human

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G02317
R;Lin, J.
Submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g1151169
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.4%; Score 262.5; DB 2; Length 794;
Best Local Similarity 30.1%; Pred. No. 5.6e-10;
Matches 69; Conservative 42; Mismatches 97; Indels 21; Gaps 5;

QY 8 VTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNY-KTLKSGQMDQL----- 59
Db 137 MSQKHLQINQTFEELRLVTDTELKLLQQTQYFIQYQESLRIOAQAQLAQSPQE 196
QY 60 NGNQSVTRQKMQQLEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWK 115
Db 197 RLSRETALQKQVSLQVLEAQLQYRVLEAEKQKTLQLLRKQQTILDELQIWK 256
QY 116 RPPIACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYKGDPIVQHRPM 175
Db 257 RRQLAGNGGPPGSLDVLQSWCKEKLAEIITWQNRQIRRAEHLCCQLPIPG-PVEEMLA 315
QY 176 LEERIVELFRLMKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLV 224
Db 316 VNATITDIISALVTSTFIEIKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 9
S5527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S5527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regulatory factor family
A;Reference number: S5527; MUID:9518889; PMID:7862987
A;Accession: S5527
A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g602354
A;Note: this is a revision to the sequence from reference S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcription factor family
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716, 'RHLHGSLPSR', '729', 'P', '731', 'ASL' <WAK>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S5527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.2%; Score 237; DB 2; Length 794;
Best Local Similarity 29.3%; Pred. No. 2.8e-08;
Matches 67; Conservative 41; Mismatches 99; Indels 22; Gaps 6;

QY 8 VTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNY-KTLKSGQMDQLNGN--- 63
Db 138 MSQKHLQINQTFEELRLVTDTELKLLQQTQYFIQYQESLRIOAQAQLAQSPQE 197
QY 64 ----QSVTRQKMQQLEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWK 115
Db 198 RLSRETALQKQVSLQVLEAQLQYRVLEAEKQKTLQLLRKQQTILDELQIWK 257
QY 116 RPPIACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYKGDPIVQHRPM 175
Db 258 RRDWRGWEAPPR-SLDVLQSWCKEKLAEIITWQNRQIRRAEHLCCQLPIPG-PVEEMLA 315

C;Accession: G02317
R;Lin, J.
Submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g1151169
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.4%; Score 262.5; DB 2; Length 794;
Best Local Similarity 30.1%; Pred. No. 5.6e-10;
Matches 69; Conservative 42; Mismatches 97; Indels 21; Gaps 5;

QY 8 VTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNY-KTLKSGQMDQL----- 59
Db 137 MSQKHLQINQTFEELRLVTDTELKLLQQTQYFIQYQESLRIOAQAQLAQSPQE 196
QY 60 NGNQSVTRQKMQQLEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWK 115
Db 197 RLSRETALQKQVSLQVLEAQLQYRVLEAEKQKTLQLLRKQQTILDELQIWK 256
QY 116 RPPIACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYKGDPIVQHRPM 175
Db 257 RRQLAGNGGPPGSLDVLQSWCKEKLAEIITWQNRQIRRAEHLCCQLPIPG-PVEEMLA 315
QY 176 LEERIVELFRLMKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLV 224
Db 316 VNATITDIISALVTSTFIEIKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 10
A54740
interleukin-4-induced transcription factor stat - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54740
R;Hou, J.; Schindler, U.; Hensel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-848 <HOU>
A;Cross-references: UNIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription regulation

Query Match 10.8%; Score 127; DB 2; Length 848;
Best Local Similarity 24.7%; Pred. No. 0.58;
Matches 59; Conservative 37; Mismatches 93; Indels 50; Gaps 9;

QY 3 PTAAVTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNYKTLKSGQMDQLNGN 62
Db 92 PLKLVAT-----FRQILQKQKAV-----MEQFRHLPPFHWKQBELFKTGLRLQHR 140
QY 63 NQSV--TQKMQQ-----LEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTL 106
Db 141 VGEIHLRLALQKQVSLQVLEAQLQYRVLEAEKQKTLQLLRKQQTILDELQIWK 196
QY 107 TDEELADWKRRPEIACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYK 166
Db 197 VLKRIQIKWKKQQLAGNAP-----FEESLAPLQERCESLVDIYSLQQLQVEGAAG 246
QY 167 DPI-VQHRPMLPEERIVELFRLMKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLV 224
Db 247 GELEPKTRASTLGRDVLRLTILVTSCLVEKQP-----PQVLKTQTKFQAGVRLFL 297

RESULT 11
I57557
DNA-Binding Protein and transcription factor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I57557
R;Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Clev
Mol. Cell. Biol. 15, 3336-3343, 1995
A;Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosp
A;Reference number: I57557; MUID:95280934; PMID:7760829
A;Accession: I57557
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-837 <RES>
A;Cross-references: UNIPROT:P52633; GB:L47650; NID:g1008876; PIDN:AAA79006.1; PID:g1008
C;Genetics:
A;Gene: STAT6
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 10.7%; Score 125.5; DB 2; Length 837;
Best Local Similarity 26.2%; Pred. No. 0.72;
Matches 61; Conservative 31; Mismatches 82; Indels 59; Gaps 10;

QY 10 EKQKMLEQ--HLQDARKRVQD-----LEQKMKVVENLQDDFDNYKTLKSGQMDQ 57
Db 106 EKKAVIEEPRHLPGPHRQKELKPTTGLRLHVRVRETRLLRESHLGPKT--GQVSLQ 163
QY 58 D-----LNGNQSVTRQKMQQLEQMLTALDQMRSSIVSELAGLLSAMEYVQKTLTDEELA 112

Db 164 NLIDPPLNGPGPS-----EDLFTILO-----GVGDELTQO-PLVLRIQ 202
QY 113 DWKRRPEIACIGPPNCLDRLENWITSLSAQSOLQTRQIKKLE-BLQOKVSYKGDPIVQ 171
Db 203 IWKRQQLAGNGTFFESLAGLQERCSLEVIYSQLHQEIGAASGELEPKT-----253
QY 172 HRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLV 224
Db 254 -RASLISRLDEVLRTLVTSFLVEKQP-----PQVLKTKQFQAGVRFL 297

RESULT 12
AE1947
Chromosome segregation protein [imported] - Nostoc sp. (strain PCC 7120)
A:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE1947
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1947
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1208 <KUR>
A:Cross-references: UNIPROT:Q8YXT3; GB:BA000019; PIDN:BA073085.1; PID:g17130474; GSPDB:G17130474
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1128
C:Superfamily: chromosome segregation protein SMC1

Query Match 10.5%; Score 122.5; DB 2; Length 1208;
Best Local Similarity 25.2%; Pred. No. 1.7;
Matches 58; Conservative 47; Mismatches 76; Indels 49; Gaps 11;
QY 5 AAVVTEKQKMLEQH--LQDARKVQDLE-QMKVVENLQDDFD--FNYKTLK-----S 52
Db 835 ATKTKTEQIQIQRETAFAEAEQRLKLENGQQLQERIQEAQQRITETQTTCTEAIN 894
QY 53 QGDMQDLNGNQ-SVTRQKMQLEQMLTALDQWRSIVSELAGLLSAMESVYQKLTDEEL 111
Db 895 RVSQQTNTTNAQITQTRAKLSELEQHLGAEKQKRDTEQEVSHLLRQOQLEWIKLEE 954
QY 112 ADWKRPEIACIGG-----PPNICLDRLENWITSLSAQSOLQTRQOI---152
Db 955 TQLKRREDTALGSQLQELVPELNPPEVDPKVDLEELQKELRSLSAK-RLQAMEPVNML 1013
QY 153 -----KGLBELOQKV-SYKGDPIVQHRPMLERIVELFRNLKMSAF 192
Db 1014 ALLEYERTQKLELSQKLTLEGE-----RTELLLR-ENFTTLAQIAF 1057

RESULT 13
G72593
hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G72593
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kato, T. DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-533 <KAW>
A:Cross-references: UNIPROT:Q9YCP2; DDBJ:AF000061; NID:g5104821; PIDN:BA080205.1; PID:dl10382966
A:Experimental source: strain K1
C:Genetics:

A:Gene: APE1216
Query Match 10.4%; Score 122; DB 2; Length 533;
Best Local Similarity 21.2%; Pred. No. 0.73;
Matches 42; Conservative 48; Mismatches 66; Indels 42; Gaps 7;
QY 8 VTEKQMLEQHLQDARKRVQDLEQMKVVEN-----LQDDF-----DENYK 48
Db 319 MSQQLQALAELESLSRSSRVEDLEARVGSVEDRLSQAEEEDISLTTSLDSLRTELEDLSTR 378
QY 49 TLKSCQDMQDLNGNQSVTRQKMQLEQMLTALDQWRSIVSELAGLLSAMESVYQKLTLD 108
Db 379 LAEAQASLEDLATLQDOVA-STLQQLQRLATAEESLQALTELASLQAEVETLQOSIVE 437
QY 109 BELADWKRRPEIACIGPPNICLDRLENWITSLSAQSOLQ-----TROQIKLEBLQOKVSY 164
Db 438 IDRLQLQRLSTVDV-----RLE--VESLGEKLVAEEKNQKQDASIEDFQSIQ- 485
QY 165 KGDPIVQHRPMLERIVE 182
Db 486 -----ELRTQLDEKRE 497

RESULT 14
A70387
conserved hypothetical protein aq_1006 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: A70387
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C. Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: A70387
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-978 <AQF>
A:Cross-references: UNIPROT:O67124; GB:AE000718; NID:g2983504; PIDN:AAC07092.1; PID:g2983504
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_1006
C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 10.4%; Score 122; DB 2; Length 978;
Best Local Similarity 23.3%; Pred. No. 1.5;
Matches 49; Conservative 38; Mismatches 81; Indels 42; Gaps 6;
QY 10 EKQKMLEQHLQDARKRVQDLEQMKVVENLQDDFDNFYKTLKSGQDMQDLNGNQSVTRQ 69
Db 234 BEKDSLERELSQVVTKLKLELENLEKEVEKLEKLEFSRKVAP-----YVPIAK 281
QY 70 KMQQLEQMLTALDQWRSIVSELAGLLSAMESVYQKLT-----DEELAD- 113
Db 282 RIEEDDKLTLEKVRKNKLTVELAVLKDELSTFAQEELNRIEAKFKFKEREKERELEHR 341
QY 114 WKRRPEIACIGPPNICLDRLENWITSLSAQSOLQTRQIKKLEBLQOKVSYKGDPIVQHR 173
Db 342 LKXKLEIKEL-----LKLSQLSSSLAKEKEVEYQAEQEFEDLSERVE-KCKKLVAET 393
QY 174 PMLERIVELFRN-----LMKSAFVVERQ 197
Db 394 EEKLEKIKELFSEEEYTSLKMKERLILVELQ 423

RESULT 15
T27075
hypothetical protein Y51A2D.16 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27075
R;McMurray, A.
submitted to the EMBL Data Library, January 1998

A;Reference number: 220307
A;Accession: T27075
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1166 <WIL>
A;Cross-references: EMBL:AL021497; PIDN:CAA16403.1; GSPDB:GN00023; CESP:Y51A2D.16
A;Experimental source: clone Y51A2D
C;Genetics:
A;Gene: CESP:Y51A2D.16
A;Map position: 5
A;Introns: 17/3; 45/1; 76/2; 156/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 948/2

Query Match 10.3%; Score 120.5; DB 2; Length 1166;
Best Local Similarity 21.4%; Pred. No. 2.3;
Matches 52; Conservative 46; Mismatches 72; Indels 73; Gaps 9;

Qy 1 NHPTAAVVTKEQ-----QMLEQHLOD-----ARKRVQDLEQKMKVVENLQDD 42
Db 430 SHVTRSLSEKNTLKAKLLE--LQDQVEAQTLELLNKGKGRLEDRDQMISNLHLKNE 487
Qy 43 FDFNYKTLKSGDMQDLNGNNSVTRQKMQLEQMLTALDOMRRSIVSELAGILLSAMEY- 101
Db 488 LENDLKTCTQCLELES-----KKLQRLREDLVLEKSRADLIGRIHSLCTTSLN 537
Qy 102 ---VQKTLTDEELAD-----WKRPEIACIGGPPNI----- 129
Db 538 GANFEKINNDELDIDNIDIMNALVAVKRRDDLRIOGNQIQELHDLKRDIEKLRSE 597
Qy 130 --CLDRLENWITSIAESQLOTROQI-----KKLELOQKVSYGDPVVOHRPMLKEERIVEL 183
Db 598 SESINESDDRVRLELTRENMTKEQVFMLOEKRLNELSTKNDI-----DMVKASIEEL 653
Qy 184 FRN 186
Db 654 NRN 656

Search completed: May 25, 2005, 17:45:30
Job time : 22.6038 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 95.284 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-31
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1157	98.7	770	1 STA3_HUMAN	P40763 homo sapien
2	1157	98.7	770	1 STA3_MOUSE	P42227 mus musculus
3	1154	98.5	770	1 STA3_RAT	P52631 rattus norv
4	1150	98.1	770	1 STA3_BOVIN	P61635 bos taurus
5	1132	96.6	771	2 Q6DW79	Q6dw79 gallus gall
6	1099	93.8	769	2 Q9PVX8	Q9pvx8 xenopus lae
7	1096	93.5	766	2 Q7ZAK3	Q7ztk3 xenopus lae
8	1011	86.3	414	2 Q7ZTS5	Q7zts5 brachydanio
9	1011	86.3	765	2 Q6DVF3	Q6dvf3 oryzias lat
10	1011	86.3	785	2 Q6NV46	Q6nv46 brachydanio
11	1011	86.3	786	2 Q6GUE7	Q6gue7 oryzias lat
12	1011	86.3	806	2 Q93599	Q93599 brachydanio
13	987	84.2	764	2 Q90T16	Q90t16 tetraodon f
14	977	83.4	767	2 Q13133	Q13133 oncorhynch
15	656	56.0	163	2 Q9N145	Q9n145 macaca mula
16	575	49.1	751	2 Q8JGN0	Q8jgn0 xenopus lae
17	573	48.9	712	2 Q6P6Q7	Q6p6q7 rattus norv
18	573	48.9	749	2 Q9QXK0	Q9qxx0 rattus norv
19	571	48.7	749	2 Q8C497	Q8c497 mus musculus
20	570	48.6	712	2 Q99K94	Q99k94 mus musculus
21	570	48.6	749	2 Q8C3V4	Q8c3v4 mus musculus
22	570	48.6	749	2 Q9D323	Q9d323 mus musculus
23	570	48.6	755	2 Q8C8M3	Q8c8m3 mus musculus
24	569	48.5	750	1 STA1_HUMAN	P42224 homo sapien
25	569	48.5	750	2 Q6BD00	Q6bd00 homo sapien
26	569	48.5	757	2 Q764M5	Q764m5 mus scrofa
27	562	48.0	749	1 STA1_MOUSE	P42225 mus musculus
28	540.5	46.1	754	2 Q13131	Q13131 oncorhynch
29	533	45.5	528	2 Q8JF08	Q8jfu8 brachydanio
30	532.5	45.4	108	2 Q704W6	Q704w6 bos taurus
31	532	45.4	749	2 Q93598	Q93598 brachydanio

32	532	45.4	749	2 Q6P943	Q6p943 brachydanio
33	531.5	45.3	718	2 Q801Y2	Q801y2 carassius a
34	520	44.4	748	1 STA4_HUMAN	Q14765 homo sapien
35	519.5	44.3	758	2 Q90Y17	Q90y17 tetraodon f
36	517.5	44.2	754	2 Q13132	Q13132 oncorhynch
37	513	43.8	657	2 Q8AW24	Q8aw24 brachydanio
38	504.5	43.0	749	1 STA4_MOUSE	F42228 mus musculus
39	504	43.0	651	2 Q7Z253	Q7z253 brachydanio
40	504	43.0	667	2 Q8AW20	Q8aw20 brachydanio
41	503.5	43.0	652	2 Q7Z277	Q7z277 brachydanio
42	503	42.9	553	2 Q8JF07	Q8jf07 brachydanio
43	503	42.9	748	2 Q6GHB2	Q6ghb2 rattus norv
44	503	42.9	1153	2 Q8JF55	Q8jfe5 brachydanio
45	491	41.9	737	2 Q90Y15	Q90y15 tetraodon f

ALIGNMENTS

RESULT 1
STA3_HUMAN
ID STA3_HUMAN STANDARD; PRT; 770 AA.
AC P40763; O14916; Q9BW54;
DT 01-FEB-1995 (Rel. 31, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=STAT3; Synonyms=APRF;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=9408062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RA Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RL Cell 77:63-71 (1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
RT "Highly conserved amino-acid sequence between murine STAT3 and a
RL revised human STAT3 sequence.";
RL Gene 213:119-124 (1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL6682 program for genomic applications, UW-
RL FHCRS, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
RC TISSUE=Kidney, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.F., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RN SEQUENCE OF 564-704 FROM N.A.
RC TISSUE=Liver;
RC Della Pietra L., Bresnan A., Pezzotti A.R., Serlupi-Crescenzi O.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RN PHOSPHORYLATION ON SERINE
RX MEDLINE=95215843; PubMed=7701321;
RA Zhang X., Bienis J., Li H.-C., Schindler C., Chen-Kiang S.;
RT "Requirement of serine phosphorylation for formation of STAT-promoter
RT complexes.";
RL Science 267:1990-1994 (1995).
RN [7]
RN INTERACTION WITH NCOAL
RX PubMed=11773079; DOI=10.1074/jbc.M11486200;
RA Graud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
RT "Functional interaction of STAT3 transcription factor with the
RT coactivator NcoA/SRC1a.";
RL J. Biol. Chem. 277:8004-8011 (2002).
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P40763-1; Sequence=Displayed;
CC Name=Del-701;
CC IsoId=P40763-2; Sequence=VSP_010474;
CC TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
CC muscle, kidney and pancreas.
CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity.
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; L29277; AAA58374.1; -
CC EMBL; AJ012463; CAAL0032.1; -
CC EMBL; AY572796; AAS66986.1; -
CC EMBL; BC000627; AAH00627.1; -
CC EMBL; BC014482; AAH14482.1; -
CC EMBL; AF029311; AAB84254.1; -
CC PIR; A54444; A54444.
CC HSP; P42227; IBG1.
CC TRANSPAC; T01493; -
CC Genew; HGNC:11364; STAT3.
CC H-InvdB; HIX0013840; -
CC MIM; 102582; -
CC GO; GO:0005737; Cytoplasm; TAS.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
CC

DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2_
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
FT VARSPIC 701 701 Missing (in isoform Del-701).
FT VARIANT 32 32 /FTId=VSP_010474.
FT VARIANT 143 143 Q -> K (in dBSNP:1803125).
FT VARIANT 143 143 M -> I.
FT CONFLICT 288 288 /FTId=VAR_018679.
FT CONFLICT 460 460 Q -> H (in Ref. 1).
FT CONFLICT 548 548 P -> S (in Ref. 1).
FT CONFLICT 561 561 K -> N (in Ref. 1).
FT CONFLICT 667 667 F -> Y (in Ref. 1).
FT CONFLICT 667 667 V -> L (in Ref. 1).
FT CONFLICT 730 730 T -> A (in Ref. 1).
SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
Query Match 98.7%; Score 1157; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.9e-65;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSGQMDQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSGQMDQDLN 189
QY 61 GNNQSVTRQKMQLEQMLTALDQMRKRSIVSELAGLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQLEQMLTALDQMRKRSIVSELAGLSAMEYVQKTLTDEELADWKRQOI 249
QY 121 ACIGGPNICLDLENWITSLSAQLOTRQOIKLEELQKYSYKGDPIVQHRPMLERI 180
DB 250 ACIGGPNICLDLENWITSLSAQLOTRQOIKLEELQKYSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 358
RESULT 2
ID STA3_MOUSE STANDARD; PRT; 770 AA.
AC P42227;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=Stat3; Synonyms=Aprf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
RP AND 632-640.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RX

RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
 RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RA "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
 RT related transcription factor involved in the gp130-mediated signaling
 RT pathway.";
 RL Cell 77:63-71 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RX TISSUE=Thymus;
 RC MEDLINE=94188718; PubMed=8140422;
 RA Zhong Z., Wen Z., Darnell J.E. Jr.;
 RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
 RL response to epidermal growth factor and interleukin-6.";
 RL Science 264:95-98 (1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RX TISSUE=Brain;
 RC MEDLINE=95014185; PubMed=7523373;
 RA Raz R., Durbin J.E., Levy D.E.;
 RT "Acute phase response factor and additional members of the interferon-
 RT stimulated gene factor 3 family integrate diverse signals from
 RT cytokines, interferons, and growth factors.";
 RL J. Biol. Chem. 269:24391-24395 (1994).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3B)
 RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
 RX MEDLINE=96016116; PubMed=7568080;
 RA Schaefer T.S., Sanders L.K., Nathans D.;
 RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
 RT form of Stat3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101 (1995).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=129/SvJ;
 RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
 RA Miyoshi K., Cui Y., Riedinger G., Lehoczy J., Zon L., Oka T.,
 RA Dewar K., Hennighausen L.;
 RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
 RT zebrafish to mouse.";
 RL Genomics 71:150-155 (2001).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=C57BL/6J, and NOD/LtJ;
 RA Davoodi-Semirani A., She J.-X.;
 RT "A mutant Stat5b with weaker DNA binding defines a key defective
 RT pathway in non-obese diabetic (NOD) mice.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnanaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [8]
 RP PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.

RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
 RA Wen Z., Zhong Z., Darnell J.E. Jr.;
 RT "Maximal activation of transcription by Stat1 and Stat3 requires both
 RT tyrosine and serine phosphorylation.";
 RL Cell 82:241-250 (1995).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
 RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
 RA Becker S., Groner B., Mueller C.W.;
 RT "Three-dimensional structure of the Stat3beta homodimer bound to
 RL DNA.";
 RL Nature 394:145-151 (1998).
 CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-response elements identified in the promoters of various
 CC acute-phase protein genes. STAT3B interacts with the N-terminal
 CC part of JUN to activate such promoters in a cooperative way.
 CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL (by similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Stat3A;
 CC IsoId=P42227-1; Sequence=Displayed;
 CC Name=Stat3B;
 CC IsoId=P42227-2; Sequence=VSP_006287;
 CC Name=Del-701;
 CC IsoId=P42227-3; Sequence=VSP_010475;
 CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
 CC kidney. STAT3B is also detected in the liver, although in a much
 CC less abundant manner.
 CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity (By similarity).
 CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; L29278; AAA37254.1; --
 DR EMBL; U06922; AAA19452.1; --
 DR EMBL; U08378; AAA56668.1; --
 DR EMBL; U30709; AAC52612.1; --
 DR EMBL; AP246978; AAL59017.1; --
 DR EMBL; AY299489; AAQ75418.1; --
 DR EMBL; AY299490; AAQ75419.1; --
 DR EMBL; BC003806; AAH03806.1; --
 DR PIR; I49508; I49508.
 DR PDB; 1BG1; X-ray; A=1-722.
 DR TRANSFAC; T01574; --
 DR MGD; MGI:103038; Stat3.
 DR CO; GO:0005737; Cytoplasm; IDA.
 DR CO; GO:0005634; C:nucleus; IDA.
 DR CO; GO:0005886; C:plasma membrane; IDA.
 DR CO; GO:0003677; F:DNA binding; IDA.
 DR CO; GO:0005515; F:protein binding; IPI.
 DR CO; GO:0016563; F:transcriptional activator activity; IDA.
 DR CO; GO:0007259; P:JAK-STAT cascade; IDA.
 DR CO; GO:0006357; P:regulation of transcription from Pol II pro. . .; IDA.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RA Strausberg R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045276; AAH45276.1; -;
DR HSSP; P42227; 1BG1.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;

Query Match 86.3%; Score 1011; DB 2; Length 414;
Best Local Similarity 84.8%; Pred. No. 2.7e-56;
Matches 195; Conservative 20; Mismatches 13; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLQEHQDARKVQDLQKMKVVENLQDDPFDNFYKTLKSGDM-QDLN 60
DB 130 HPTGTVTEKQMLQEHQDARKVQDLQKMKVVENLQDDPFDNFYKTLKSGELSDLN 189
QY 61 GNNQ-SVTRQKMQQLQMLTALDQMRSSIVSELAGLLSAMYVQKTLTDEELADWKRRPE 119
DB 190 GNSQAATROKMAQLEQLSALDQRRQIVTEMGGLLTAMDYVQKLTDEELADWKRRQ 249
QY 120 IACIGGPNICLDRLNWTLSAESQLQTRQIKLEELQKQVYKGDPIVQHRPMLER 179
DB 250 IACIGGPNICLDRLTWTLSAESQLQTRQIKLEELQKQVYKGDPIIHRPALEEK 309
QY 180 IVELFRNLKSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 229
DB 310 IVDLFRNLKSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 359

RESULT 9
Q6DVF3 PRELIMINARY; PRT; 765 AA.
ID Q6DVF3
AC Q6DVF3
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Signal transducer and activation of transcription factor 3.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY639947; AAT64912.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;
Query Match 86.3%; Score 1011; DB 2; Length 765;
Best Local Similarity 84.8%; Pred. No. 5.2e-56;
Matches 195; Conservative 19; Mismatches 14; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLQEHQDARKVQDLQKMKVVENLQDDPFDNFYKTLKSGDM-QDLN 60
DB 130 HPTGTVTEKQMLQEHQDARKVQDLQKMKVVENLQDDPFDNFYKTLKSGELSDLN 189
QY 61 GNNQ-SVTRQKMQQLQMLTALDQMRSSIVSELAGLLSAMYVQKTLTDEELADWKRRPE 119
DB 190 GNSQAATROKMAQLEQLSALDQRRQIVTEMGGLLTAMDYVQKLTDEELADWKRRQ 249
QY 120 IACIGGPNICLDRLNWTLSAESQLQTRQIKLEELQKQVYKGDPIVQHRPMLER 179
DB 250 IACIGGPNICLDRLTWTLSAESQLQTRQIKLEELQKQVYKGDPIIHRPALEEK 309
QY 180 IVELFRNLKSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 229
DB 310 IVDLFRNLKSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 359
RESULT 10
Q6GUE7 PRELIMINARY; PRT; 785 AA.
ID Q6GUE7
AC Q6GUE7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Signal transducer and activator of transcription 3 isoform 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT4364.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.

DR Pfam; PF02864; STAT bind; 1.
DR Pfam; PF02865; STAT int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;

Query Match 86.3%; Score 1011; DB 2; Length 785;
Best Local Similarity 84.8%; Pred. No. 5.3e-56;
Matches 195; Conservative 19; Mismatches 14; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEQHLQDARKEVDLEQKMKVVENLQDDFDNFYKTLKSQGM-QDIN 60
Db 130 HPTGTVTEKQMLEHNLQDARKVQDMQKMKLENLQDDFDNFYKTLKSQGM-QDIN 189
QY 61 GNNQ-SVTRQKQKQMLEQMLTALDQMRSSIVSELAGLLSAMEYVQKLTDEELADWKRPE 119
Db 190 GNSQAATRQKQKQMLEQMLTALDQMRSSIVSELAGLLSAMEYVQKLTDEELADWKRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLOTRQIQIKKLEELQKQSYKGDPIVHRPMLER 179
Db 250 IACIGGPPNICLDRLNWTSLAESQLOTRQIQIKKLEELQKQSYKGDPIVHRPMLER 309
QY 180 IVELFRNLMSAFVVERQPCMPHDPRLVIKTGQVFTTKVRLLVKPEL 229
Db 310 IVDLFRNLMSAFVVERQPCMPHDPRLVIKTGQVFTTKVRLLVKPEL 359

RESULT 11
Q6NV46 ID Q6NV46 PRELIMINARY; PRT; 786 AA.
AC Q6NV46; 093599; PRELIMINARY; PRT; 806 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udell T.B., Toshitsugu S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska A., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068320; AH68320.1; -;
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF001017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;

Query Match 86.3%; Score 1011; DB 2; Length 786;
Best Local Similarity 84.8%; Pred. No. 5.4e-56;
Matches 195; Conservative 20; Mismatches 13; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGM-QDIN 60
Db 130 HPTGTVTEKQMLEHNLQDARKRVQDLEQKMKLENLQDDFDNFYKTLKSQGM-QDIN 189
QY 61 GNNQ-SVTRQKQKQMLEQMLTALDQMRSSIVSELAGLLSAMEYVQKLTDEELADWKRPE 119
Db 190 GNSQAATRQKQKQMLEQMLTALDQMRSSIVSELAGLLSAMEYVQKLTDEELADWKRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLOTRQIQIKKLEELQKQSYKGDPIVHRPMLER 179
Db 250 IACIGGPPNICLDRLNWTSLAESQLOTRQIQIKKLEELQKQSYKGDPIVHRPMLER 309
QY 180 IVELFRNLMSAFVVERQPCMPHDPRLVIKTGQVFTTKVRLLVKPEL 229
Db 310 IVDLFRNLMSAFVVERQPCMPHDPRLVIKTGQVFTTKVRLLVKPEL 359

RESULT 12
O93599 ID O93599 PRELIMINARY; PRT; 806 AA.
AC O93599; 093599; PRELIMINARY; PRT; 806 AA.
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oates A.C.;
RL Thesis (1998), University of Melbourne, Australia.
DR EMBL; AJ005693; CAA06677.1; -;
DR HSSP; P42227; 1BG1.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF001017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match 86.3%; Score 1011; DB 2; Length 806;
Best Local Similarity 84.8%; Pred. No. 5.5e-56;


```
Matches 195; Conservative 20; Mismatches 13; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 60
Db 130 HPTGTVTEKQMLELNLQDARKRVQDMQKMKLENLQDDFDNFYKTLKSQGLSODLN 189
QY 61 GNNQ-SVTRQKQMLELNLQDARKRVQDMQKMKLENLQDDFDNFYKTLKSQGLSODLN 119
Db 190 GNSQAARQKMAQLQDLRRQIVTEMAGLLSAMDVFQKRLTDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKVSYSKGDPIVQHRPMLER 179
Db 250 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKVSYSKGDPIVQHRPMLER 309
QY 180 IVELFRLNLMKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLMKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 359

RESULT 13
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF02864; STAT_alpha; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFE18BEFD8BE CRC64;

Query Match 84.2%; Score 987; DB 2; Length 764;
Best Local Similarity 83.5%; Pred. No. 1.7e-54;
Matches 192; Conservative 20; Mismatches 16; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 60
Db 130 NPSGTVTEKQMLELNLQDARKRVQDMQKMKLENLQDDFDNFYKTLKSQGLSODLN 189
QY 61 GNNQ-SVTRQKQMLELNLQDARKRVQDMQKMKLENLQDDFDNFYKTLKSQGLSODLN 119
Db 190 GNSQAARQKMAQLQDLRRQIVTEMAGLLSAMDVFQKRLTDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKVSYSKGDPIVQHRPMLER 179
Db 250 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKVSYSKGDPIVQHRPMLER 309
QY 180 IVELFRLNLMKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLMKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 359

RESULT 14
Q13133 PRELIMINARY; PRT; 767 AA.
AC Q13133;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
GN NamesrbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8023;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match 83.4%; Score 977; DB 2; Length 767;
Best Local Similarity 81.4%; Pred. No. 7.4e-54;
Matches 188; Conservative 24; Mismatches 17; Indels 2; Gaps 2;
QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDL 59
Db 129 SHPSGTVTEKQMLELNLQDARKRVQDMQKMKLENLQDDFDNFYKTLKSQGLSODM 188
QY 60 GNNQ-SVTRQKQMLELNLQDARKRVQDMQKMKLENLQDDFDNFYKTLKSQGLSODM 118
Db 189 NGNSQAARQKMAQLQDLRRQIVTEMAGLLSAMDVFQKRLTDEELADWKRRQ 248
QY 119 ETACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKVSYSKGDPIVQHRPMLER 178
Db 249 QIACIGGPPKICLDRLETWITSLSGRIQLQIRQIKKLEELQKVSYSKGDPIVQHRPMLER 308
QY 179 RIVELFRLNLMKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 229
Db 309 KIVDLFRNLMKSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 359

RESULT 15
Q9N145 PRELIMINARY; PRT; 163 AA.
AC Q9N145;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (fragment).
GN Name=STAT3;
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AF227560; AAF73401.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
FT NON_TER 1
FT TER 163
SQ SEQUENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;

Query Match 56.0%; Score 656; DB 2; Length 163;
Best Local Similarity 98.4%; Pred.No.3.le-34;
Matches 126; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 102 VQKLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESOLQTRQIQKLEELQOK 161
Db 1 VQKLTDEELADWKRRQIQIACIGGPPNICLDRLNWTSLAESOLQTRQIQKLEELQOK 60

Qy 162 VSYKGDPIVQHRPMLERIVELFRNLKSAFVVERQPCMPHDPDRPLVKTGVQFTTKVR 221
Db 61 VSYKGDPIVQHRPMLERIVELFRNLKSAFVVERQPCMPHDPDRPLVKTGVQFTTKVR 120

Qy 222 LLVKFPPEL 229
Db 121 LLVKFPPEL 128

Search completed: May 25, 2005, 17:43:45
Job time : 96.284 secs